

10/525907

## SEQUENCE LISTING

DT06 Rec'd PCT/PTO 25 FEB 2005

<110> Kroger, Burkhard  
 Zelder, Oskar  
 Kolpprogge, Corinna  
 Schroder, Hartwig  
 Hafner, Stefan

<120> Method for Production by Fermentation of Sulphur-Containing Fine Chemicals (metF)

<130> 13111-00005-US

<150> PCT/EP 2003/009451  
 <151> 2003-08-26

<150> DE 102 39 308.7  
 <151> 2002-08-27

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<170> PatentIn version 3.3

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Ser Val Ala Glu Leu Arg Asn Ile Ile Gly Gln Tyr Ala Asp Ala Gly	
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&lt;213&gt; Aquifex aeolicus

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225 230 235 240Asp Lys Pro Glu Glu Val Lys Lys Ile Gly Ile Glu Phe Ala Ile Asn  
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 gcc att ctc aac gag tac cgc gca cat ggc atc cgc cat atc gtc gcg 288  
  
 Ala Ile Leu Asn Glu Tyr Arg Ala His Gly Ile Arg His Ile Val Ala  
 85 . 90 . 95 .  
  
 ctg cgc ggc gat ctg ccg tcc ggc atg ggc gaa gtc ggc gag ctg cgc 336  
 Leu Arg Gly Asp Leu Pro Ser Gly Met Gly Glu Val Gly Glu Leu Arg  
 100 . 105 . 110 .  
  
 tat gcg tcg gaa ctg gtg agc ttt atc cgc gcc gaa ttc ggc gac tgg 384  
 Tyr Ala Ser Glu Leu Val Ser Phe Ile Arg Ala Glu Phe Gly Asp Trp  
 115 . 120 . 125 .  
  
 ttc tgc atc gag gtg gcc ggc tat ccg gaa tac cac ccg cag tcg cgc 432  
 Phe Cys Ile Glu Val Ala Gly Tyr Pro Glu Tyr His Pro Gln Ser Arg  
 130 . 135 . 140 .  
  
 tcg ccg cgt cag gat ctg gaa aac ttc gcc cgc aag gtg aag gcc ggc 480  
 Ser Pro Arg Gln Asp Leu Glu Asn Phe Ala Arg Lys Val Lys Ala Gly  
 145 . 150 . 155 . 160 .  
  
 gcc aat tcg gcg atc aca cag tac ttc ttc aat gca gac gcg tat ttc 528  
 Ala Asn Ser Ala Ile Thr Gln Tyr Phe Phe Asn Ala Asp Ala Tyr Phe  
 165 . 170 . 175 .  
  
 cgt ttc gtc gac gac gcg aga aag ctc ggc gtg gac gtg ccg atc gtg 576  
 Arg Phe Val Asp Asp Ala Arg Lys Leu Gly Val Asp Val Pro Ile Val

180

185

190

ccg ggc atc atg ccg atc acg aac ttc tcg cag ctg atg cgt ttc tcg 624  
 Pro Gly Ile Met Pro Ile Thr Asn Phe Ser Gln Leu Met Arg Phe Ser  
 195 200 205

gag atg tgc ggc gct gaa gtg cca cgc tgg atc gcg cgc cg<sup>g</sup> ctg gaa 672  
 Glu Met Cys Gly Ala Glu Val Pro Arg Trp Ile Ala Arg Arg Leu Glu  
 210 215 220

agc ttc ggc gac gat cgc gag tca att cgc gcg ttc ggg ctg gat gtg 720  
 Ser Phe Gly Asp Asp Arg Glu Ser Ile Arg Ala Phe Gly Leu Asp Val  
 225 230 235 240

gtg acg gac ctg tgc agg cgt ctg atc gat gcg aag gtg ccg ggc ctg 768  
 Val Thr Asp Leu Cys Arg Arg Leu Ile Asp Ala Lys Val Pro Gly Leu  
 245 250 255

cac ttc tac acg cta aac ggc gca gcg gcg acc aag gcg atc tgc gaa 816  
 His Phe Tyr Thr Leu Asn Gly Ala Ala Ala Thr Lys Ala Ile Cys Glu  
 260 265 270

cg<sup>g</sup> ttg aac gtt taa 831  
 Arg Leu Asn Val  
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<210> 10  
 <211> 276  
 <212> PRT  
 <213> Burkholderia cepacia

<400> 10  
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Glu Gly Val Asp Lys Leu Arg Ala Thr Arg Ala Gln Leu Ala Thr Leu  
 20 25 30

Lys Pro Lys Phe Val Ser Val Thr Phe Gly Ala Gly Gly Ser Thr Gln  
 35 40 45

Gln Gly Thr Leu Asp Thr Val Val Asp Met Ala Lys Glu Gly Leu Glu  
 50 55 60

Ala Ala Pro His Val Ser Cys Ile Gly Ser Ser Lys Glu Ser Leu Arg  
 65 70 75 80

Ala Ile Leu Asn Glu Tyr Arg Ala His Gly Ile Arg His Ile Val Ala  
 85 90 95

Leu Arg Gly Asp Leu Pro Ser Gly Met Gly Glu Val Gly Glu Leu Arg  
 100 105 110

Tyr Ala Ser Glu Leu Val Ser Phe Ile Arg Ala Glu Phe Gly Asp Trp  
 115 120 125

Phe Cys Ile Glu Val Ala Gly Tyr Pro Glu Tyr His Pro Gln Ser Arg  
 130 135 140

Ser Pro Arg Gln Asp Leu Glu Asn Phe Ala Arg Lys Val Lys Ala Gly  
 145 150 155 160  
 Ala Asn Ser Ala Ile Thr Gln Tyr Phe Phe Asn Ala Asp Ala Tyr Phe  
 165 170 175  
 Arg Phe Val Asp Asp Ala Arg Lys Leu Gly Val Asp Val Pro Ile Val  
 180 185 190  
 Pro Gly Ile Met Pro Ile Thr Asn Phe Ser Gln Leu Met Arg Phe Ser  
 195 200 205  
 Glu Met Cys Gly Ala Glu Val Pro Arg Trp Ile Ala Arg Arg Leu Glu  
 210 215 220  
 Ser Phe Gly Asp Asp Arg Glu Ser Ile Arg Ala Phe Gly Leu Asp Val  
 225 230 235 240  
 Val Thr Asp Leu Cys Arg Arg Leu Ile Asp Ala Lys Val Pro Gly Leu  
 245 250 255  
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 260 265 270  
 Arg Leu Asn Val  
 275

<210> 11  
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 <212> DNA  
 <213> Nitrosomonas europaea

<220>  
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 <222> (1)...(843)  
 <223> RNE02657

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 1 5 10 15

ccg ccg cag aca ccg gaa ggc atg gaa aag ctg cgg gca acg cgc ata 96  
 Pro Pro Gln Thr Pro Glu Gly Met Glu Lys Leu Arg Ala Thr Arg Ile  
 20 25 30

cag ctt gct cag ttc aat ccg aag ttt ttc tcg gtg acg ttt ggt gcc 144  
 Gln Leu Ala Gln Phe Asn Pro Lys Phe Phe Ser Val Thr Phe Gly Ala  
 35 40 45

ggc gga tcc act cgt gaa cgc acg ctc gaa acc gtg ctg gaa att cag 192  
 Gly Gly Ser Thr Arg Glu Arg Thr Leu Glu Thr Val Leu Glu Ile Gln  
 50 55 60

gca gaa ggc tat ccg gta gcg ccc cat ctt tcc tgt atc ggc tcc acg 240  
 Ala Glu Gly Tyr Pro Val Ala Pro His Leu Ser Cys Ile Gly Ser Thr  
 65 70 75 80

cgt gac aat atc cgt tcg atc ctt gag aaa tat cac agt cac ggt atc	288
Arg Asp Asn Ile Arg Ser Ile Leu Glu Lys Tyr His Ser His Gly Ile	
85 90 95	
agc cgc att gtg gcg cta cgt ggt gat tta ccc tcc ggc atg gcg cag	336
Ser Arg Ile Val Ala Leu Arg Gly Asp Leu Pro Ser Gly Met Ala Gln	
100 105 110	
gcg gga gaa ttc cgc tac gcc aac gag ctg gta gca ttt atc cgc aag	384
Ala Gly Glu Phe Arg Tyr Ala Asn Glu Leu Val Ala Phe Ile Arg Lys	
115 120 125	
gag ttc ggt gat acc ttc tgg atc gaa gtg gcg gct tat ccg gaa tat	432
Glu Phe Gly Asp Thr Phe Trp Ile Glu Val Ala Ala Tyr Pro Glu Tyr	
130 135 140	
cat cca caa gcc cgc tcc gct ctg gag gat ttc acc aat ttc aga cga	480
His Pro Gln Ala Arg Ser Ala Leu Glu Asp Phe Thr Asn Phe Arg Arg	
145 150 155 160	
aaa gtc gaa gca ggt tcc aat gca gcg att acc cag ttt ttc tat aac	528
Lys Val Glu Ala Gly Ser Asn Ala Ala Thr Gln Phe Phe Tyr Asn	
165 170 175	
gtg gat gcc tat ctg cat ttc gta gag atg tgt gaa gct gcg gat ctg	576
Val Asp Ala Tyr Leu His Phe Val Glu Met Cys Glu Ala Ala Asp Leu	
180 185 190	
aat atc ccg atc gtt ccc ggc atc atg ccg atc agc aaa ttt tct caa	624
Asn Ile Pro Ile Val Pro Gly Ile Met Pro Ile Ser Lys Phe Ser Gln	
195 200 205	
ctg gca aga ttt tcg gat ggc tgt gga gca gaa att cca cgc tgg att	672
Leu Ala Arg Phe Ser Asp Gly Cys Gly Ala Glu Ile Pro Arg Trp Ile	
210 215 220	
cgc aga aaa ctg gaa agc ttc ggt gat gat att ccg tct atc cag gca	720
Arg Arg Lys Leu Glu Ser Phe Gly Asp Asp Ile Pro Ser Ile Gln Ala	
225 230 235 240	
ttc ggg ctg gat gtc gtc aca gcg tta tgt gct cgt ctg ctg gaa gcc	768
Phe Gly Leu Asp Val Val Thr Ala Leu Cys Ala Arg Leu Leu Glu Ala	
245 250 255	
ggc gca ccc ggc ctg cat ttc tac aca ctc aac tcc gcc gta cta ccc	816
Gly Ala Pro Gly Leu His Phe Tyr Thr Leu Asn Ser Ala Val Leu Pro	
260 265 270	
aca aaa atc tgg caa cgc ctg ggg tta tag	846
Thr Lys Ile Trp Gln Arg Leu Gly Leu	
275 280	

<210> 12  
 <211> 281  
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 <213> Nitrosomonas europaea

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 Met Gln Ser Gln Lys Lys Phe Thr Pro Thr Phe Ser Phe Glu Phe Phe  
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 Gln Leu Ala Gln Phe Asn Pro Lys Phe Phe Ser Val Thr Phe Gly Ala  
 35 40 45  
 Gly Gly Ser Thr Arg Glu Arg Thr Leu Glu Thr Val Leu Glu Ile Gln  
 50 55 60  
 Ala Glu Gly Tyr Pro Val Ala Pro His Leu Ser Cys Ile Gly Ser Thr  
 65 70 75 80  
 Arg Asp Asn Ile Arg Ser Ile Leu Glu Lys Tyr His Ser His Gly Ile  
 85 90 95  
 Ser Arg Ile Val Ala Leu Arg Gly Asp Leu Pro Ser Gly Met Ala Gln  
 100 105 110  
 Ala Gly Glu Phe Arg Tyr Ala Asn Glu Leu Val Ala Phe Ile Arg Lys  
 115 120 125  
 Glu Phe Gly Asp Thr Phe Trp Ile Glu Val Ala Ala Tyr Pro Glu Tyr  
 130 135 140  
 His Pro Gln Ala Arg Ser Ala Leu Glu Asp Phe Thr Asn Phe Arg Arg  
 145 150 155 160  
 Lys Val Glu Ala Gly Ser Asn Ala Ala Ile Thr Gln Phe Phe Tyr Asn  
 165 170 175  
 Val Asp Ala Tyr Leu His Phe Val Glu Met Cys Glu Ala Ala Asp Leu  
 180 185 190  
 Asn Ile Pro Ile Val Pro Gly Ile Met Pro Ile Ser Lys Phe Ser Gln  
 195 200 205  
 Leu Ala Arg Phe Ser Asp Gly Cys Gly Ala Glu Ile Pro Arg Trp Ile  
 210 215 220  
 Arg Arg Lys Leu Glu Ser Phe Gly Asp Asp Ile Pro Ser Ile Gln Ala  
 225 230 235 240  
 Phe Gly Leu Asp Val Val Thr Ala Leu Cys Ala Arg Leu Leu Glu Ala  
 245 250 255  
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 260 265 270  
 Thr Lys Ile Trp Gln Arg Leu Gly Leu  
 275 280

<210> 13  
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 <213> *Pseudomonas aeruginosa*

<220>  
 <221> CDS  
 <222> (1)..(870)  
 <223> RPA03308

<400> 13

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1															15	
agc	tcc	gag	ttc	ttc	ccg	gct	aag	acc	gag	gcc	ggc	cat	gaa	aag	ctg	96
Ser	Phe	Glu	Phe	Phe	Pro	Ala	Lys	Thr	Glu	Ala	Gly	His	Glu	Lys	Leu	
20															30	
ttg	gcc	acc	gcc	cgc	aac	ctg	gct	ggc	tac	aag	ccc	gac	ttc	ttc	tcc	144
Leu	Ala	Thr	Ala	Arg	Asn	Ieu	Ala	Gly	Tyr	Lys	Pro	Asp	Phe	Phe	Ser	
35															45	
tgc	acc	tac	ggc	gcc	ggc	gga	tcc	acc	cgc	gac	cgc	acg	ttg	agt	acc	192
Cys	Thr	Tyr	Gly	Ala	Gly	Gly	Ser	Thr	Arg	Asp	Arg	Thr	Leu	Ser	Thr	
50															60	
gtg	ctg	caa	ctg	gac	ggc	gag	gtg	aag	gtg	ccg	acc	gct	ccg	cac	ctg	240
Val	Leu	Gln	Leu	Asp	Gly	Glu	Val	Lys	Val	Pro	Thr	Ala	Pro	His	Leu	
65															80	
tcc	tgt	gtc	ggc	gac	tcg	aaa	gcc	gag	ttg	cgc	gaa	ctg	ctc	ggc	cgc	288
Ser	Cys	Val	Gly	Asp	Ser	Lys	Ala	Glu	Leu	Arg	Glu	Leu	Leu	Gly	Arg	
85															95	
tac	cgc	gag	gcc	ggc	atc	cgc	cgc	atc	gtc	gcc	ctg	cgc	ggc	gac	ctg	336
Tyr	Arg	Glu	Ala	Gly	Ile	Arg	Arg	Ile	Val	Ala	Leu	Arg	Gly	Asp	Leu	
100															110	
ccg	tcg	ggc	atg	ggc	atg	gcc	agc	ggc	gaa	ctg	cgc	tac	gcc	aac	gaa	384
Pro	Ser	Gly	Met	Gly	Met	Ala	Ser	Gly	Glu	Leu	Arg	Tyr	Ala	Asn	Glu	
115															125	
ctg	gtg	gac	ttc	atc	cgc	acc	gag	acc	ggc	gac	cac	ttc	cac	atc	gag	432
Leu	Val	Asp	Phe	Ile	Arg	Thr	Glu	Thr	Gly	Asp	His	Phe	His	Ile	Glu	
130															140	
gtc	gcc	gcc	tat	ccg	gag	gtc	cac	ccc	cag	gct	cgc	agc	ttc	gag	gat	480
Val	Ala	Ala	Tyr	Pro	Glu	Val	His	Pro	Gln	Ala	Arg	Ser	Phe	Glu	Asp	
145															160	
gac	ctg	gct	aat	ttc	gtg	cgc	aag	gtg	aag	gcc	ggc	gcc	agc	agc	gcc	528
Asp	Leu	Ala	Asn	Phe	Val	Arg	Lys	Val	Lys	Ala	Gly	Ala	Ser	Ser	Ala	
165															175	
atc	acc	cag	tac	ttc	ttc	aac	gcc	gat	gcc	tat	ttc	tac	ttc	gtc	gag	576
Ile	Thr	Gln	Tyr	Phe	Phe	Asn	Ala	Asp	Ala	Tyr	Phe	Tyr	Phe	Val	Glu	
180															190	
cgg	gtc	gcc	aag	ctc	ggc	gtg	gac	atc	ccg	gtg	gtc	ccc	ggc	atc	atg	624
Arg	Val	Ala	Lys	Leu	Gly	Val	Asp	Ile	Pro	Val	Val	Pro	Gly	Ile	Met	
195															205	
ccg	atc	acc	aac	tac	tcc	aag	ctg	gct	cgc	ttc	tcc	gac	gcc	tgc	ggc	672

Pro Ile Thr Asn Tyr Ser Lys Leu Ala Arg Phe Ser Asp Ala Cys Gly  
 210 215 220

gcc gaa ctg ccg cgc tgg atc cgc aag caa ctg gaa gcc tac ggc gac 720  
 Ala Glu Leu Pro Arg Trp Ile Arg Lys Gln Leu Glu Ala Tyr Gly Asp  
 225 230 235 240

gac agc cgc agc atc cag gcc ttc ggc gag cag gtc atc agc gag atg 768  
 Asp Ser Arg Ser Ile Gln Ala Phe Gly Glu Gln Val Ile Ser Glu Met  
 245 250 255

tgc gaa cgc ctg ctg gag ggc ggc gca ccg gga ctg cat ttc tat act 816  
 Cys Glu Arg Leu Leu Glu Gly Ala Pro Gly Leu His Phe Tyr Thr  
 260 265 270

ttg aac cag gcc gat ccg agc ctg gcg atc tgg aag aat ctc cag ctg 864  
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 275 280 285

cca cgc tga 873  
 Pro Arg  
 290

<210> 14  
 <211> 290  
 <212> PRT  
 <213> Pseudomonas aeruginosa

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Ser Phe Glu Phe Phe Pro Ala Lys Thr Glu Ala Gly His Glu Lys Leu  
 20 25 30

Leu Ala Thr Ala Arg Asn Leu Ala Gly Tyr Lys Pro Asp Phe Phe Ser  
 35 40 45

Cys Thr Tyr Gly Ala Gly Gly Ser Thr Arg Asp Arg Thr Leu Ser Thr  
 50 55 60

Val Leu Gln Leu Asp Gly Glu Val Lys Val Pro Thr Ala Pro His Leu  
 65 70 75 80

Ser Cys Val Gly Asp Ser Lys Ala Glu Leu Arg Glu Leu Leu Gly Arg  
 85 90 95

Tyr Arg Glu Ala Gly Ile Arg Arg Ile Val Ala Leu Arg Gly Asp Leu  
 100 105 110

Pro Ser Gly Met Gly Met Ala Ser Gly Glu Leu Arg Tyr Ala Asn Glu  
 115 120 125

Leu Val Asp Phe Ile Arg Thr Glu Thr Gly Asp His Phe His Ile Glu  
 130 135 140

Val Ala Ala Tyr Pro Glu Val His Pro Gln Ala Arg Ser Phe Glu Asp  
 145 150 155 160

Asp Leu Ala Asn Phe Val Arg Lys Val Lys Ala Gly Ala Ser Ser Ala  
 165 170 175

Ile Thr Gln Tyr Phe Phe Asn Ala Asp Ala Tyr Phe Tyr Phe Val Glu  
 180 185 190

Arg Val Ala Lys Leu Gly Val Asp Ile Pro Val Val Pro Gly Ile Met  
 195 200 205

Pro Ile Thr Asn Tyr Ser Lys Leu Ala Arg Phe Ser Asp Ala Cys Gly  
 210 215 220

Ala Glu Leu Pro Arg Trp Ile Arg Lys Gln Leu Glu Ala Tyr Gly Asp  
 225 230 235 240

Asp Ser Arg Ser Ile Gln Ala Phe Gly Glu Gln Val Ile Ser Glu Met  
 245 250 255

Cys Glu Arg Leu Leu Glu Gly Gly Ala Pro Gly Leu His Phe Tyr Thr  
 260 265 270

Leu Asn Gln Ala Asp Pro Ser Leu Ala Ile Trp Lys Asn Leu Gln Leu  
 275 280 285

Pro Arg  
 290

<210> 15  
 <211> 828  
 <212> DNA  
 <213> Xylella almond

<220>  
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 <222> (1)...(825)  
 <223> RXFX00359

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 1 5 10 15

cgc gca cag ttg gac agg aca gca aac cgg cta cgc gca ttc gca cca 96  
 Arg Ala Gln Leu Asp Arg Thr Ala Asn Arg Leu Arg Ala Phe Ala Pro  
 20 25 30

gaa tac gtc tcc tgc acc ttc ggc gcc ggt ggc tcc aca ctc agt tac 144  
 Glu Tyr Val Ser Cys Thr Phe Gly Ala Gly Gly Ser Thr Leu Ser Tyr  
 35 40 45

acc tca gaa aca gtg cgc cat ctc agc caa cac cac ggc ttt gac gcc 192  
 Thr Ser Glu Thr Val Arg His Leu Ser Gln His His Gly Phe Asp Ala  
 50 55 60

gca ccg cat ctg tcc tgt gtg ggc ggc agt cgc caa gaa atc cgc gaa 240  
 Ala Pro His Leu Ser Cys Val Gly Gly Ser Arg Gln Glu Ile Arg Glu  
 65 70 75 80

ctt ctc aaa ctg tac cgc gcg att ggc tgc caa cgc atc gtg gcg cta	288
Leu Leu Lys Leu Tyr Arg Ala Ile Gly Cys Gln Arg Ile Val Ala Leu	
85 90 95	
cgc ggc gat ctc ccc tcg ggc atg ggc cac ccc ggc gac ctc cgc tac	336
Arg Gly Asp Leu Pro Ser Gly Met Gly His Pro Gly Asp Leu Arg Tyr	
100 105 110	
gca gct gac ctg att acc ttc atc cgt acc gag cat ggc gat cac ttc	384
Ala Ala Asp Leu Ile Thr Phe Ile Arg Thr Glu His Gly Asp His Phe	
115 120 125	
cac cta gag atc ggc gca tac ccg gaa acc cac cca caa gcc agc aac	432
His Leu Glu Ile Gly Ala Tyr Pro Glu Thr His Pro Gln Ala Ser Asn	
130 135 140	
aca ctg aac gac ctt cac tat ttc aaa gcc aaa gcc gat gca ggc gcc	480
Thr Leu Asn Asp Leu His Tyr Phe Lys Ala Lys Ala Asp Ala Gly Ala	
145 150 155 160	
gat gcg gca atc act caa tac ttt tat aac cca gac gcc tat ttc cac	528
Asp Ala Ala Ile Thr Gln Tyr Phe Tyr Asn Pro Asp Ala Tyr Phe His	
165 170 175	
ttc gtc gac gca gtg cag cgc ctg ggc gtc acc atc ccc att gtt gcc	576
Phe Val Asp Ala Val Gln Arg Leu Gly Val Thr Ile Pro Ile Val Ala	
180 185 190	
gga gtc atg ccc atc tcc aac ttt gac cag ttg cgc cat ttc tcc gaa	624
Gly Val Met Pro Ile Ser Asn Phe Asp Gln Leu Arg His Phe Ser Glu	
195 200 205	
caa tgc ggc gcc gaa ata ccc cgc tgg att aca aaa aaa atg cag gct	672
Gln Cys Gly Ala Glu Ile Pro Arg Trp Ile Thr Lys Lys Met Gln Ala	
210 215 220	
tac ggc gac gac acc aaa tcg ata cgc gcg ttc ggt gcc gac gtc gtg	720
Tyr Gly Asp Asp Thr Lys Ser Ile Arg Ala Phe Gly Ala Asp Val Val	
225 230 235 240	
acc gca tta tgt gag cgg cta atc gct ggc ggc gca ccg ggg ctg cac	768
Thr Ala Leu Cys Glu Arg Leu Ile Ala Gly Gly Ala Pro Gly Leu His	
245 250 255	
ttc tac acg ctc aac cta gcc aaa cca agc acc caa gtg ctg caa cgc	816
Phe Tyr Thr Leu Asn Leu Ala Lys Pro Ser Thr Gln Val Leu Gln Arg	
260 265 270	
tta ggc tat tga	828
Leu Gly Tyr	
275	

<210> 16  
<211> 275  
<212> PRT  
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<400> 16

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 20 25 30

Glu Tyr Val Ser Cys Thr Phe Gly Ala Gly Gly Ser Thr Leu Ser Tyr  
 35 40 45

Thr Ser Glu Thr Val Arg His Leu Ser Gln His His Gly Phe Asp Ala  
 50 55 60

Ala Pro His Leu Ser Cys Val Gly Gly Ser Arg Gln Glu Ile Arg Glu  
 65 70 75 80

Leu Leu Lys Leu Tyr Arg Ala Ile Gly Cys Gln Arg Ile Val Ala Leu  
 85 90 95

Arg Gly Asp Leu Pro Ser Gly Met Gly His Pro Gly Asp Leu Arg Tyr  
 100 105 110

Ala Ala Asp Leu Ile Thr Phe Ile Arg Thr Glu His Gly Asp His Phe  
 115 120 125

His Leu Glu Ile Gly Ala Tyr Pro Glu Thr His Pro Gln Ala Ser Asn  
 130 135 140

Thr Leu Asn Asp Leu His Tyr Phe Lys Ala Lys Ala Asp Ala Gly Ala  
 145 150 155 160

Asp Ala Ala Ile Thr Gln Tyr Phe Tyr Asn Pro Asp Ala Tyr Phe His  
 165 170 175

Phe Val Asp Ala Val Gln Arg Leu Gly Val Thr Ile Pro Ile Val Ala  
 180 185 190

Gly Val Met Pro Ile Ser Asn Phe Asp Gln Leu Arg His Phe Ser Glu  
 195 200 205

Gln Cys Gly Ala Glu Ile Pro Arg Trp Ile Thr Lys Lys Met Gln Ala  
 210 215 220

Tyr Gly Asp Asp Thr Lys Ser Ile Arg Ala Phe Gly Ala Asp Val Val  
 225 230 235 240

Thr Ala Leu Cys Glu Arg Leu Ile Ala Gly Gly Ala Pro Gly Leu His  
 245 250 255

Phe Tyr Thr Leu Asn Leu Ala Lys Pro Ser Thr Gln Val Leu Gln Arg  
 260 265 270

Leu Gly Tyr  
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<210> 17  
 <211> 828  
 <212> DNA  
 <213> Xylella oleander

<220>  
 <221> CDS  
 <222> (1)..(825)  
 <223> RXFY01676

<400> 17

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1	5								10					15		

cgc gca cag ttg gac agg aca gca aac cgg cta cgc gca ttc gca cca 96

Arg	Ala	Gln	Leu	Asp	Arg	Thr	Ala	Asn	Arg	Leu	Arg	Ala	Phe	Ala	Pro	
20	25								30							

gaa tac gtc tcc tgc acc ttgc ggc gcc ggc tcc aca ctc agt tac 144

Glu	Tyr	Val	Ser	Cys	Thr	Phe	Gly	Ala	Gly	Gly	Ser	Thr	Leu	Ser	Tyr	
35	40								45							

acc tca gaa aca gtg cgc cat ctc agt caa cac cac ggc ttt gac acc 192

Thr	Ser	Glu	Thr	Val	Arg	His	Leu	Ser	Gln	His	His	Gly	Phe	Asp	Thr	
50	55								60							

gca ccg cat ctg tcc tgt gtg ggc .ggc agt cgc caa gaa atc cgc gaa 240

Ala	Pro	His	Leu	Ser	Cys	Val	Gly	Gly	Ser	Arg	Gln	Glu	Ile	Arg	Glu	
65	70							75	80							

ctt ctc aaa ctg tac cgc gcg att ggc tgc caa cgc atc gtg gcg cta 288

Leu	Leu	Lys	Leu	Tyr	Arg	Ala	Ile	Gly	Cys	Gln	Arg	Ile	Val	Ala	Leu	
85	90							95								

cgc ggc gat ctc ccc tcg ggc atg ggc cac ccc ggc gac ctc cgc tac 336

Arg	Gly	Asp	Leu	Pro	Ser	Gly	Met	Gly	His	Pro	Gly	Asp	Leu	Arg	Tyr	
100	105							110								

gca gct gac ctg att acc ttc atc cgt gcc gag cat ggc gat cac ttc 384

Ala	Ala	Asp	Leu	Ile	Thr	Phe	Ile	Arg	Ala	Glu	His	Gly	Asp	His	Phe	
115	120							125								

cac cta gag atc ggc gca tac ccg gaa acc cac cca caa gcc agc aac 432

His	Leu	Glu	Ile	Gly	Ala	Tyr	Pro	Glu	Thr	His	Pro	Gln	Ala	Ser	Asn	
130	135							140								

aca ctg aac gac ctt cac tat ttc aaa gcc aaa gcc gat gca ggc gcc 480

Thr	Leu	Asn	Asp	Leu	His	Tyr	Phe	Lys	Ala	Lys	Ala	Asp	Ala	Gly	Ala	
145	150							155	160							

gat gcg gca atc act caa tac ttt tac aac cca gac gcc tat ttc cac 528

Asp	Ala	Ala	Ile	Thr	Gln	Tyr	Phe	Tyr	Asn	Pro	Asp	Ala	Tyr	Phe	His	
165	170							175								

ttc gtc gac gca gtg cag cgc ctg ggc gtc acc atc ccc att gtt gcc 576

Phe	Val	Asp	Ala	Val	Gln	Arg	Leu	Gly	Val	Thr	Ile	Pro	Ile	Val	Ala	
180	185							190								

gga gtc atg ccc atc tcc aac ttt gac cag ttg cgc cat ttc tcc gaa 624

Gly	Val	Met	Pro	Ile	Ser	Asn	Phe	Asp	Gln	Leu	Arg	His	Phe	Ser	Glu	
195	200							205								

caa tgc ggc gcc gaa ata ccc cgc tgg att aca aaa aaa atg cag gct 672  
 Gln Cys Gly Ala Glu Ile Pro Arg Trp Ile Thr Lys Lys Met Gln Ala  
 210 215 220

tac ggc gat gac acc aaa tcg ata cgc gcg ttc ggt gcc gac gtc gtg 720  
 Tyr Gly Asp Asp Thr Lys Ser Ile Arg Ala Phe Gly Ala Asp Val Val  
 225 230 235 240

acc gca cta tgt gag cgg cta atc gct ggc gca ccg ggg ctg cac 768  
 Thr Ala Leu Cys Glu Arg Leu Ile Ala Gly Gly Ala Pro Gly Leu His  
 245 250 255

ttc tac acg ctc aac cta gcc aaa cca agc acc caa gtg ctg caa cgc 816  
 Phe Tyr Thr Leu Asn Leu Ala Lys Pro Ser Thr Gln Val Leu Gln Arg  
 260 265 270

tta ggc tat tga 828  
 Leu Gly Tyr  
 275

<210> 18  
 <211> 275  
 <212> PRT  
 <213> Xylella oleander

<400> 18  
 Met Ile Pro Ile Ser Phe Glu Phe Tyr Pro Pro Lys Asn Asp Asp Gln  
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Arg Ala Gln Leu Asp Arg Thr Ala Asn Arg Leu Arg Ala Phe Ala Pro  
 20 25 30

Glu Tyr Val Ser Cys Thr Phe Gly Ala Gly Gly Ser Thr Leu Ser Tyr  
 35 40 45

Thr Ser Glu Thr Val Arg His Leu Ser Gln His His Gly Phe Asp Thr  
 50 55 60

Ala Pro His Leu Ser Cys Val Gly Gly Ser Arg Gln Glu Ile Arg Glu  
 65 70 75 80

Leu Leu Lys Leu Tyr Arg Ala Ile Gly Cys Gln Arg Ile Val Ala Leu  
 85 90 95

Arg Gly Asp Leu Pro Ser Gly Met Gly His Pro Gly Asp Leu Arg Tyr  
 100 105 110

Ala Ala Asp Leu Ile Thr Phe Ile Arg Ala Glu His Gly Asp His Phe  
 115 120 125

His Leu Glu Ile Gly Ala Tyr Pro Glu Thr His Pro Gln Ala Ser Asn  
 130 135 140

Thr Leu Asn Asp Leu His Tyr Phe Lys Ala Lys Ala Asp Ala Gly Ala  
 145 150 155 160

Asp Ala Ala Ile Thr Gln Tyr Phe Tyr Asn Pro Asp Ala Tyr Phe His

165

170

175

Phe Val Asp Ala Val Gln Arg Leu Gly Val Thr Ile Pro Ile Val Ala  
 180 185 190

Gly Val Met Pro Ile Ser Asn Phe Asp Gln Leu Arg His Phe Ser Glu  
 195 200 205

Gln Cys Gly Ala Glu Ile Pro Arg Trp Ile Thr Lys Lys Met Gln Ala  
 210 215 220

Tyr Gly Asp Asp Thr Lys Ser Ile Arg Ala Phe Gly Ala Asp Val Val  
 225 230 235 240

Thr Ala Leu Cys Glu Arg Leu Ile Ala Gly Gly Ala Pro Gly Leu His  
 245 250 255

Phe Tyr Thr Leu Asn Leu Ala Lys Pro Ser Thr Gln Val Leu Gln Arg  
 260 265 270

Leu Gly Tyr  
 275

&lt;210&gt; 19

&lt;211&gt; 846

&lt;212&gt; DNA

&lt;213&gt; Pseudomonas fluorescens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(843)

&lt;223&gt; RPU04845

&lt;400&gt; 19

atg tcc caa gac cgt cgc tac agc ttc gag ttc ttc ccg acc aag acc 48  
 Met Ser Gln Asp Arg Arg Tyr Ser Phe Glu Phe Phe Pro Thr Lys Thr  
 1 5 10 15

gat gct ggg cat gaa aaa ctg ctc gcc act gcc cgt cag ctg gcc acc 96  
 Asp Ala Gly His Glu Lys Leu Leu Ala Thr Ala Arg Gln Leu Ala Thr  
 20 25 30

tat aag cct gac ttc ttt tcc tgc acc tac ggc gct ggc ggt tcg acc 144  
 Tyr Lys Pro Asp Phe Phe Ser Cys Thr Tyr Gly Ala Gly Gly Ser Thr  
 35 40 45

cgt gac cgc acg ctg aac acc gtt ctg cag ctg gaa agc gaa gtc aaa 192  
 Arg Asp Arg Thr Leu Asn Thr Val Leu Gln Leu Glu Ser Glu Val Lys  
 50 55 60

atc ccc gcc gca ccg cac ctg tcg tgc gtc ggc gac agc aag gac gac 240  
 Ile Pro Ala Ala Pro His Leu Ser Cys Val Gly Asp Ser Lys Asp Asp  
 65 70 75 80

ctg cgc ggc ctg ctg aac gag tac aag gac ggc ggc atc aag cgc atc 288  
 Leu Arg Gly Leu Leu Asn Glu Tyr Lys Ala Ala Gly Ile Lys Arg Ile  
 85 90 95

gtc gcc ctg cgc ggt gac ctg ccg tcc ggc atg ggc atg acc agc ggc	336
Val Ala Leu Arg Gly Asp Leu Pro Ser Gly Met Gly Met Thr Ser Gly	
100 105 110	
gag ctg cgt cac gcc aat gaa ctg gtt gaa ttc att cgt gaa gaa acc	384
Glu Leu Arg His Ala Asn Glu Leu Val Glu Phe Ile Arg Glu Glu Thr	
115 120 125	
ggc aat cat ttc cac atc gaa gtc gcc gac tac ccg gag atg cat ccg	432
Gly Asn His Phe His Ile Glu Val Ala Ala Tyr Pro Glu Met His Pro	
130 135 140	
caa gcg cgc aac tac gaa gac gat ctc gcc aac ttc gtg cgc aag gcc	480
Gln Ala Arg Asn Tyr Glu Asp Asp Leu Ala Asn Phe Val Arg Lys Ala	
145 150 155 160	
cgt gcc ggc gac agc gcg atc acc cag tac ttc ttc aac gcc gac	528
Arg Ala Gly Ala Asp Ser Ala Ile Thr Gln Tyr Phe Phe Asn Ala Asp	
165 170 175	
agc tac ttc tac ttc gtc gac cgt ttg cag gcg ctg ggc gtg gac att	576
Ser Tyr Phe Tyr Phe Val Asp Arg Leu Gln Ala Leu Gly Val Asp Ile	
180 185 190	
ccg gtg gta ccg ggg atc atg ccg atc acc aac tac agc aaa ctc gcg	624
Pro Val Val Pro Gly Ile Met Pro Ile Thr Asn Tyr Ser Lys Leu Ala	
195 200 205	
cgc ttc tcc gat gcc tgc ggt gcg gaa atc ccg cgc tgg atc cgc aag	672
Arg Phe Ser Asp Ala Cys Gly Ala Glu Ile Pro Arg Trp Ile Arg Lys	
210 215 220	
cag ctg gaa gcc tac ggc gat gac agc caa agc att cag cgc ttt ggc	720
Gln Leu Glu Ala Tyr Gly Asp Asp Ser Gln Ser Ile Gln Arg Phe Gly	
225 230 235 240	
gaa caa gtc gtc acg gaa atg tgc gaa cgc ctg ctg caa ggc ggc gcg	768
Glu Gln Val Val Thr Glu Met Cys Glu Arg Leu Leu Gln Gly Gly Ala	
245 250 255	
ccc ggc ctg cac ttc tat tcc atg aac cag gcc gaa cca agc ctg gcg	816
Pro Gly Leu His Phe Tyr Ser Met Asn Gln Ala Glu Pro Ser Leu Ala	
260 265 270	
atc tgg aac aac ctg aag ctg ccg cgc taa	846
Ile Trp Asn Asn Leu Lys Leu Pro Arg	
275 280	

<210> 20  
 <211> 281  
 <212> PRT  
 <213> Pseudomonas fluorescens

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 Asp Ala Gly His Glu Lys Leu Leu Ala Thr Ala Arg Gln Leu Ala Thr  
 20 25 30

Tyr Lys Pro Asp Phe Phe Ser Cys Thr Tyr Gly Ala Gly Gly Ser Thr  
 35 40 45

Arg Asp Arg Thr Leu Asn Thr Val Leu Gln Leu Glu Ser Glu Val Lys  
 50 55 60

Ile Pro Ala Ala Pro His Leu Ser Cys Val Gly Asp Ser Lys Asp Asp  
 65 70 75 80

Leu Arg Gly Leu Leu Asn Glu Tyr Lys Ala Ala Gly Ile Lys Arg Ile  
 85 90 95

Val Ala Leu Arg Gly Asp Leu Pro Ser Gly Met Gly Met Thr Ser Gly  
 100 105 110

Glu Leu Arg His Ala Asn Glu Leu Val Glu Phe Ile Arg Glu Glu Thr  
 115 120 125

Gly Asn His Phe His Ile Glu Val Ala Ala Tyr Pro Glu Met His Pro  
 130 135 140

Gln Ala Arg Asn Tyr Glu Asp Asp Leu Ala Asn Phe Val Arg Lys Ala  
 145 150 155 160

Arg Ala Gly Ala Asp Ser Ala Ile Thr Gln Tyr Phe Phe Asn Ala Asp  
 165 170 175

Ser Tyr Phe Tyr Phe Val Asp Arg Leu Gln Ala Leu Gly Val Asp Ile  
 180 185 190

Pro Val Val Pro Gly Ile Met Pro Ile Thr Asn Tyr Ser Lys Leu Ala  
 195 200 205

Arg Phe Ser Asp Ala Cys Gly Ala Glu Ile Pro Arg Trp Ile Arg Lys  
 210 215 220

Gln Leu Glu Ala Tyr Gly Asp Asp Ser Gln Ser Ile Gln Arg Phe Gly  
 225 230 235 240

Glu Gln Val Val Thr Glu Met Cys Glu Arg Leu Leu Gln Gly Gly Ala  
 245 250 255

Pro Gly Leu His Phe Tyr Ser Met Asn Gln Ala Glu Pro Ser Leu Ala  
 260 265 270

Ile Trp Asn Asn Leu Lys Leu Pro Arg  
 275 280

<210> 21  
 <211> 1812  
 <212> DNA  
 <213> Schizosaccharomyces pombe

<220>  
 <221> CDS  
 <222> (1)...(1809)  
 <223> RSO01645

<400> 21

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Met Lys Ile Ser Asp Lys Leu Leu His Pro Asp Trp Lys Glu Lys Val	
1 5 10 15	
act tac agt tat gaa ttt ttt cct cca aaa acg agc act ggt gtc caa	96
Thr Tyr Ser Tyr Glu Phe Phe Pro Pro Lys Thr Ser Thr Gly Val Gln	
20 25 30	
aat ctt tac aat cgt ata gat cgc atg aag act tgg ggt cgt ccc atg	144
Asn Leu Tyr Asn Arg Ile Asp Arg Met Lys Thr Trp Gly Arg Pro Met	
35 40 45	
ttt gtc gat gtg act tgg ggt gct ggt act tct tca gaa ctg act	192
Phe Val Asp Val Thr Trp Gly Ala Gly Gly Thr Ser Ser Glu Leu Thr	
50 55 60	
cct gga atc gtt aat gta att caa aca gat ttt gaa gtg gat act tgc	240
Pro Gly Ile Val Asn Val Ile Gln Thr Asp Phe Glu Val Asp Thr Cys	
65 70 75 80	
atg cat ttg act tgt acg aac atg tcc aca gaa atg att gac gca gct	288
Met His Leu Thr Cys Thr Asn Met Ser Thr Glu Met Ile Asp Ala Ala	
85 90 95	
ttg aaa cgg gct cat gaa aca ggg tgt cgt aac ata ttg gcc ctt aga	336
Leu Lys Arg Ala His Glu Thr Gly Cys Arg Asn Ile Leu Ala Leu Arg	
100 105 110	
ggg gat cct gtt aaa gat aca gac tgg act gaa ggc gaa agt gga ttc	384
Gly Asp Pro Val Lys Asp Thr Asp Trp Thr Glu Gly Glu Ser Gly Phe	
115 120 125	
cgg tat gct tca gac tta gtt aga tat att cgc aca cat tat aat gat	432
Arg Tyr Ala Ser Asp Leu Val Arg Tyr Ile Arg Thr His Tyr Asn Asp	
130 135 140	
gaa ttc tgt att ggt gta gct ggc tat cca gaa gga tat tca cca gat	480
Glu Phe Cys Ile Gly Val Ala Gly Tyr Pro Glu Gly Tyr Ser Pro Asp	
145 150 155 160	
gat gac att gat gaa agc ata aag cat ctg aaa tta aaa gtc gat gaa	528
Asp Asp Ile Asp Glu Ser Ile Lys His Leu Lys Leu Lys Val Asp Glu	
165 170 175	
ggg gct gat ttt atc gtt act caa atg ttt tat gat gta gac aat ttt	576
Gly Ala Asp Phe Ile Val Thr Gln Met Phe Tyr Asp Val Asp Asn Phe	
180 185 190	
atc gca tgg gtc gat aaa gtg cgt gca gca gga ata aat atc cct ata	624
Ile Ala Trp Val Asp Lys Val Arg Ala Ala Gly Ile Asn Ile Pro Ile	
195 200 205	
ttt ccg ggc att atg cct att cag gca tgg gat tcc ttt att cgg aga	672
Phe Pro Gly Ile Met Pro Ile Gln Ala Trp Asp Ser Phe Ile Arg Arg	
210 215 220	
gcg aaa tgg agc ggt gtt aaa att ccc cag cat ttt atg gat act cta	720
Ala Lys Trp Ser Gly Val Lys Ile Pro Gln His Phe Met Asp Thr Leu	
225 230 235 240	

gtc cca gtt aaa gac gat gat gaa gga gtc cgt gag cgt ggt gtt gag		768	
Val Pro Val Lys Asp Asp Asp Glu Gly Val Arg Glu Arg Gly Val Glu			
245	250	255	
ctc ata gtc gaa atg tgc cgt aag ctt ata gct agt ggc att acg aga		816	
Leu Ile Val Glu Met Cys Arg Lys Leu Ile Ala Ser Gly Ile Thr Arg			
260	265	270	
ctt cat ttt tac act atg aat tta gaa aag gcc gtt aaa atg att att		864	
Leu His Phe Tyr Thr Met Asn Leu Glu Lys Ala Val Lys Met Ile Ile			
275	280	285	
gaa cga tta ggt tta tta gat gaa aac ttg gct cct ata gtg gat act		912	
Glu Arg Leu Gly Leu Leu Asp Glu Asn Leu Ala Pro Ile Val Asp Thr			
290	295	300	
aat aac gtc gag tta acc aat gct tcc agt caa gat cgt cgg ata aat		960	
Asn Asn Val Glu Leu Thr Asn Ala Ser Ser Gln Asp Arg Arg Ile Asn			
305	310	315	320
gaa ggt gta cgg ccc att ttc tgg cgc act cgt aat gaa agt tat gtc		1008	
Glu Gly Val Arg Pro Ile Phe Trp Arg Thr Arg Asn Glu Ser Tyr Val			
325	330	335	
tcg cgt act gat cag tgg gac gaa tta ccg cat ggt cgt tgg ggt gac		1056	
Ser Arg Thr Asp Gln Trp Asp Glu Leu Pro His Gly Arg Trp Gly Asp			
340	345	350	
tct cgt agc cct gct ttt ggc gaa ttt gat gct att aga tat ggt ctt		1104	
Ser Arg Ser Pro Ala Phe Gly Glu Phe Asp Ala Ile Arg Tyr Gly Leu			
355	360	365	
cgt atg tct ccc aag gag atc aca aca tcg tgg ggg tct cct aaa tct		1152	
Arg Met Ser Pro Lys Glu Ile Thr Ser Trp Gly Ser Pro Lys Ser			
370	375	380	
tac tcg gaa atc ggc gat ttg ttt gcc agg tac tgt gaa aaa aag att		1200	
Tyr Ser Glu Ile Gly Asp Leu Phe Ala Arg Tyr Cys Glu Lys Lys Ile			
385	390	395	400
agc tcc ctc cct tgg agt gat ctt ccc ata tcc gat gaa gcc gac ttg		1248	
Ser Ser Leu Pro Trp Ser Asp Leu Pro Ile Ser Asp Glu Ala Asp Leu			
405	410	415	
att cgg gat caa ctt cta agt atg aat aga aac gct ttc ctt act ata		1296	
Ile Arg Asp Gln Leu Leu Ser Met Asn Arg Asn Ala Phe Leu Thr Ile			
420	425	430	
aat tct caa cct gct ctt aac ggc gaa aag agt tca cat cct gtt ttt		1344	
Asn Ser Gln Pro Ala Leu Asn Gly Glu Lys Ser Ser His Pro Val Phe			
435	440	445	
gga tgg gga cca cct aat ggt tat gtt ttc caa aaa cca tac gtt gag		1392	
Gly Trp Gly Pro Pro Asn Gly Tyr Val Phe Gln Lys Pro Tyr Val Glu			
450	455	460	
ttt ttc gtt cac ccc tca ctc ttg aat gaa ctc aaa gaa acc gtt aaa		1440	
Phe Phe Val His Pro Ser Leu Leu Asn Glu Leu Lys Glu Thr Val Lys			
465	470	475	480

aag ctt aat tca gtt tcc tac ttt gtt aca aac aag aat gga gac.ttg	1488
Lys Leu Asn Ser Val Ser Tyr Phe Val Thr Asn Lys Asn Gly Asp Leu	
485 490 495	
gat acc aac tca caa tat gag att cca aat gcg gtt aca tgg ggt gtt	1536
Asp Thr Asn Ser Gln Tyr Glu Ile Pro Asn Ala Val Thr Trp Gly Val	
500 505 510	
ttc cct aat cgt gag att atc caa cct act att gtc gag tca acc tct	1584
Phe Pro Asn Arg Glu Ile Ile Gln Pro Thr Ile Val Glu Ser Thr Ser	
515 520 525	
ttt ctt gct tgg aaa gat gaa gcc tat tca ttg ggc atg gaa tgg gct	1632
Phe Leu Ala Trp Lys Asp Glu Ala Tyr Ser Leu Gly Met Glu Trp Ala	
530 535 540	
aat gca tat agc cct gat tca att tct cgt aaa ctt ttg gtt tct.atg	1680
Asn Ala Tyr Ser Pro Asp Ser Ile Ser Arg Lys Leu Leu Val Ser Met	
545 550 555 560	
atg aag gaa tgg ttc ctt tgt gtc ata gtt gat aac gat ttt caa aat	1728
Met Lys Glu Trp Phe Leu Cys Val Ile Val Asp Asn Asp Phe Gln Asn	
565 570 575	
ggg caa tct ttg ttt gat gtt ttt aac aaa atg aga tct tta aaa gac	1776
Gly Gln Ser Leu Phe Asp Val Phe Asn Lys Met Arg Ser Leu Lys Asp	
580 585 590	
atc cat cct gag cta tat tat gca aat gca tca taa	1812
Ile His Pro Glu Leu Tyr Tyr Ala Asn Ala Ser	
595 600	

<210> 22  
 <211> 603  
 <212> PRT  
 <213> Schizosaccharomyces pombe

<400> 22	
Met Lys Ile Ser Asp Lys Leu Leu His Pro Asp Trp Lys Glu Lys Val	
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Thr Tyr Ser Tyr Glu Phe Phe Pro Pro Lys Thr Ser Thr Gly Val Gln	
20 25 30	
Asn Leu Tyr Asn Arg Ile Asp Arg Met Lys Thr Trp Gly Arg Pro Met	
35 40 45	
Phe Val Asp Val Thr Trp Gly Ala Gly Gly Thr Ser Ser Glu Leu Thr	
50 55 60	
Pro Gly Ile Val Asn Val Ile Gln Thr Asp Phe Glu Val Asp Thr Cys	
65 70 75 80	
Met His Leu Thr Cys Thr Asn Met Ser Thr Glu Met Ile Asp Ala Ala	
85 90 95	
Leu Lys Arg Ala His Glu Thr Gly Cys Arg Asn Ile Leu Ala Leu Arg	
100 105 110	

Gly Asp Pro Val Lys Asp Thr Asp Trp Thr Glu Gly Glu Ser Gly Phe  
 115 120 125

Arg Tyr Ala Ser Asp Leu Val Arg Tyr Ile Arg Thr His Tyr Asn Asp  
 130 135 140

Glu Phe Cys Ile Gly Val Ala Gly Tyr Pro Glu Gly Tyr Ser Pro Asp  
 145 150 155 160

Asp Asp Ile Asp Glu Ser Ile Lys His Leu Lys Leu Lys Val Asp Glu  
 165 170 175

Gly Ala Asp Phe Ile Val Thr Gln Met Phe Tyr Asp Val Asp Asn Phe  
 180 185 190

Ile Ala Trp Val Asp Lys Val Arg Ala Ala Gly Ile Asn Ile Pro Ile  
 195 200 205

Phe Pro Gly Ile Met Pro Ile Gln Ala Trp Asp Ser Phe Ile Arg Arg  
 210 215 220

Ala Lys Trp Ser Gly Val Lys Ile Pro Gln His Phe Met Asp Thr Leu  
 225 230 235 240

Val Pro Val Lys Asp Asp Glu Gly Val Arg Glu Arg Gly Val Glu  
 245 250 255

Leu Ile Val Glu Met Cys Arg Lys Leu Ile Ala Ser Gly Ile Thr Arg  
 260 265 270

Leu His Phe Tyr Thr Met Asn Leu Glu Lys Ala Val Lys Met Ile Ile  
 275 280 285

Glu Arg Leu Gly Leu Leu Asp Glu Asn Leu Ala Pro Ile Val Asp Thr  
 290 295 300

Asn Asn Val Glu Leu Thr Asn Ala Ser Ser Gln Asp Arg Arg Ile Asn  
 305 310 315 320

Glu Gly Val Arg Pro Ile Phe Trp Arg Thr Arg Asn Glu Ser Tyr Val  
 325 330 335

Ser Arg Thr Asp Gln Trp Asp Glu Leu Pro His Gly Arg Trp Gly Asp  
 340 345 350

Ser Arg Ser Pro Ala Phe Gly Glu Phe Asp Ala Ile Arg Tyr Gly Leu  
 355 360 365

Arg Met Ser Pro Lys Glu Ile Thr Thr Ser Trp Gly Ser Pro Lys Ser  
 370 375 380

Tyr Ser Glu Ile Gly Asp Leu Phe Ala Arg Tyr Cys Glu Lys Lys Ile  
 385 390 395 400

Ser Ser Leu Pro Trp Ser Asp Leu Pro Ile Ser Asp Glu Ala Asp Leu  
 405 410 415

Ile Arg Asp Gln Leu Leu Ser Met Asn Arg Asn Ala Phe Leu Thr Ile  
 420 425 430

Asn Ser Gln Pro Ala Leu Asn Gly Glu Lys Ser Ser His Pro Val Phe  
 435 440 445

Gly Trp Gly Pro Pro Asn Gly Tyr Val Phe Gln Lys Pro Tyr Val Glu  
 450 455 460

Phe Phe Val His Pro Ser Leu Leu Asn Glu Leu Lys Glu Thr Val Lys  
 465 470 475 480

Lys Leu Asn Ser Val Ser Tyr Phe Val Thr Asn Lys Asn Gly Asp Leu  
 485 490 495

Asp Thr Asn Ser Gln Tyr Glu Ile Pro Asn Ala Val Thr Trp Gly Val  
 500 505 510

Phe Pro Asn Arg Glu Ile Ile Gln Pro Thr Ile Val Glu Ser Thr Ser  
 515 520 525

Phe Leu Ala Trp Lys Asp Glu Ala Tyr Ser Leu Gly Met Glu Trp Ala  
 530 535 540

Asn Ala Tyr Ser Pro Asp Ser Ile Ser Arg Lys Leu Leu Val Ser Met  
 545 550 555 560

Met Lys Glu Trp Phe Leu Cys Val Ile Val Asp Asn Asp Phe Gln Asn  
 565 570 575

Gly Gln Ser Leu Phe Asp Val Phe Asn Lys Met Arg Ser Leu Lys Asp  
 580 585 590

Ile His Pro Glu Leu Tyr Tyr Ala Asn Ala Ser  
 595 600

<210> 23  
 <211> 1800  
 <212> DNA  
 <213> *Saccharomyces cerevisiae*

<220>  
 <221> CDS  
 <222> (1)...(1797)  
 <223> RSC08323

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 Met Lys Ile Thr Glu Lys Leu Glu Gln His Arg Gln Thr Ser Gly Lys  
 1 5 10 15

ccc act tac tca ttc gag tac ttc gtc ccg aag act aca caa ggt gta 96  
 Pro Thr Tyr Ser Phe Glu Tyr Phe Val Pro Lys Thr Thr Gln Gly Val  
 20 25 30

cag aac ctg tat gac cggt atg gac cggt atg tac gag gct tct ttg ccc 144  
 Gln Asn Leu Tyr Asp Arg Met Asp Arg Met Tyr Glu Ala Ser Leu Pro  
 35 40 45

caa ttt att gac atc acc tgg aat gca ggc ggt gga cggt ttg tca cat 192

Gln	Phe	Ile	Asp	Ile	Thr	Trp	Asn	Ala	Gly	Gly	Gly	Arg	Leu	Ser	His	
50																
ctg	tcc	acg	gac	ttg	gtt	gcg	aca	gcg	cag	tct	gtg	ctt	ggt	ttg	gaa	240
Leu	Ser	Thr	Asp	Leu	Val	Ala	Thr	Ala	Gln	Ser	Val	Leu	Gly	Leu	Glu	
65																
acg	tgc	atg	cac	ctt	acc	tgc	acc	aat	atg	ccc	att	tcg	atg	att	gac	288
Thr	Cys	Met	His	Leu	Thr	Cys	Thr	Asn	Met	Pro	Ile	Ser	Met	Ile	Asp	
85																
gac	gct	tta	gaa	aac	gct	tat	cac	tcc	ggt	tgc	cag	aac	atc	cta	gcg	336
Asp	Ala	Leu	Glu	Asn	Ala	Tyr	His	Ser	Gly	Cys	Gln	Asn	Ile	Leu	Ala	
100																
ctg	aga	gga	gat	cct	cct	agg	gac	gca	gaa	aac	tgg	act	ccc	gtt	gaa	384
Leu	Arg	Gly	Asp	Pro	Pro	Arg	Asp	Ala	Glu	Asn	Trp	Thr	Pro	Val	Glu	
115																
ggt	ggc	ttc	cag	tat	gcc	aag	gac	ttg	att	aag	tat	atc	aag	tcc	aag	432
Gly	Gly	Phe	Gln	Tyr	Ala	Lys	Asp	Leu	Ile	Lys	Tyr	Ile	Lys	Ser	Lys	
130																
tac	ggt	gac	cat	ttc	gct	atc	ggc	gtt	gcc	ggc	tac	ccg	gag	tgc	cat	480
Tyr	Gly	Asp	His	Phe	Ala	Ile	Gly	Val	Ala	Gly	Tyr	Pro	Glu	Cys	His	
145																
ccg	gag	ttg	cct	aac	aaa	gac	gtg	aag	ctt	gat	ctc	gag	tat	ttg	agc	528
Pro	Glu	Leu	Pro	Asn	Lys	Asp	Val	Lys	Leu	Asp	Leu	Glu	Tyr	Leu	Ser	
165																
aga	aga	tcg	acc	ggc	ggc	gac	ttc	atc	atc	act	cag	atg	ttt	tac	gat	576
Arg	Arg	Ser	Thr	Gly	Gly	Asp	Phe	Ile	Ile	Thr	Gln	Met	Phe	Tyr	Asp	
180																
gtt	gat	aat	tta	ctc	aac	tgg	tgt	tcc	caa	gtt	aga	gct	gcg	ggc	atg	624
Val	Asp	Asn	Leu	Leu	Asn	Trp	Cys	Ser	Gln	Val	Arg	Ala	Ala	Gly	Met	
195																
gac	gtg	ccc	att	att	ccc	ggg	atc	atg	ccg	atc	act	acc	tac	gct	gcc	672
Asp	Val	Pro	Ile	Ile	Pro	Gly	Ile	Met	Pro	Ile	Thr	Thr	Tyr	Ala	Ala	
210																
ttc	ttg	aga	agg	atc	caa	tgg	ggc	caa	atc	tcc	atc	cct	caa	cat	ttc	720
Phe	Leu	Arg	Arg	Ile	Gln	Trp	Gly	Gln	Ile	Ser	Ile	Pro	Gln	His	Phe	
225																
tcg	tcc	cga	ttg	gat	cct	atc	aag	gac	gat	gac	gag	ttg	gtc	cgt	gat	768
Ser	Ser	Arg	Leu	Asp	Pro	Ile	Lys	Asp	Asp	Asp	Glu	Leu	Val	Arg	Asp	
245																
atc	gga	act	aac	ttg	atc	gtg	gaa	atg	tgt	caa	aaa	ttg	ctc	gac	agt	816
Ile	Gly	Thr	Asn	Leu	Ile	Val	Glu	Met	Cys	Gln	Lys	Leu	Leu	Asp	Ser	
260																
ggt	tac	gtt	tct	cac	ttg	cac	atc	acc	atg	aac	ttg	gaa	aaa	gct		864
Gly	Tyr	Val	Ser	His	Leu	His	Ile	Tyr	Thr	Met	Asn	Leu	Glu	Lys	Ala	
275																
cct	ctc	atg	att	ctg	gaa	aga	ttg	aac	att	cta	cct	acg	gaa	tca	gag	912

Pro	Leu	Met	Ile	Leu	Glu	Arg	Leu	Asn	Ile	Leu	Pro	Thr	Glu	Ser	Glu	
290				295					300							
ttc aat gca cat cca ttg gcc gtg ttg cca tgg aga aaa tct ttg aat															960	
Phe	Asn	Ala	His	Pro	Leu	Ala	Val	Leu	Pro	Trp	Arg	Lys	Ser	Leu	Asn	
305				310				315				320				
cca aag cgt aaa aac gag gaa gtc aga cct atc ttc tgg aag aga aga															1008	
Pro	Lys	Arg	Lys	Asn	Glu	Glu	Val	Arg	Pro	Ile	Phe	Trp	Lys	Arg	Arg	
325					330				335							
cct tac tcc tat gtc gca aga acc tct caa tgg gcc gtg gac gaa ttc															1056	
Pro	Tyr	Ser	Tyr	Val	Ala	Arg	Thr	Ser	Gln	Trp	Ala	Val	Asp	Glu	Phe	
340				345					350							
ccc aac ggt aga ttc ggt gat tcg tct tct cct gcg ttc ggt gac ttg															1104	
Pro	Asn	Gly	Arg	Phe	Gly	Asp	Ser	Ser	Pro	Ala	Phe	Gly	Asp	Leu		
355				360				365								
gat ctg tgt ggt tca gac ttg atc agg caa tca gcg aac aaa tgt ctc															1152	
Asp	Leu	Cys	Gly	Ser	Asp	Leu	Ile	Arg	Gln	Ser	Ala	Asn	Lys	Cys	Leu	
370				375				380								
gaa tta tgg tcc acc cct act tcc atc aac gac gtc gcc ttc ttg gtc															1200	
Glu	Leu	Trp	Ser	Thr	Pro	Thr	Ser	Ile	Asn	Asp	Val	Ala	Phe	Leu	Val	
385				390				395			400					
atc aac tac ttg aat gga aac ttg aag tgt tta cct tgg agt gat atc															1248	
Ile	Asn	Tyr	Leu	Asn	Gly	Asn	Leu	Lys	Cys	Leu	Pro	Trp	Ser	Asp	Ile	
405				410					415							
ccc atc aat gat gaa ata aat cca atc aaa gca cac ttg att gag ctg															1296	
Pro	Ile	Asn	Asp	Glu	Ile	Asn	Pro	Ile	Lys	Ala	His	Ile	Glu	Leu		
420				425				430								
aac cag cat tct atc atc act ata aac tct caa cct caa gtc aac ggc															1344	
Asn	Gln	His	Ser	Ile	Ile	Thr	Ile	Asn	Ser	Gln	Pro	Gln	Val	Asn	Gly	
435				440				445								
att agg tcc aat gac aaa att cat ggt tgg gga ccc aag gat ggt tac															1392	
Ile	Arg	Ser	Asn	Asp	Lys	Ile	His	Gly	Trp	Gly	Pro	Lys	Asp	Gly	Tyr	
450				455				460								
gtt tac cag aag caa tat ttg gaa ttt atg ttg ccc aag act aag ttg															1440	
Val	Tyr	Gln	Lys	Gln	Tyr	Leu	Glu	Phe	Met	Leu	Pro	Lys	Thr	Lys	Leu	
465				470				475			480					
ccc aag ttg att gac acc ttg aaa aac aat gag ttc ttg acc tac ttc															1488	
Pro	Lys	Leu	Ile	Asp	Thr	Leu	Lys	Asn	Asn	Glu	Phe	Leu	Thr	Tyr	Phe	
485				490					495							
gcc atc gac tct caa ggt gac ctg cta agt aat cat cca gac aac tcc															1536	
Ala	Ile	Asp	Ser	Gln	Gly	Asp	Leu	Leu	Ser	Asn	His	Pro	Asp	Asn	Ser	
500				505				510								
aag tcc aac gct gtg act tgg ggt att ttc ccc ggc aga gaa att ctt															1584	
Lys	Ser	Asn	Ala	Val	Thr	Trp	Gly	Ile	Phe	Pro	Gly	Arg	Glu	Ile	Leu	
515				520				525								
caa cct acc att gtc gag aaa att tcg ttc tta gcg tgg aag gag gag															1632	

Gln Pro Thr Ile Val Glu Lys Ile Ser Phe Leu Ala Trp Lys Glu Glu  
 530 535 540

ttc tat cat atc ttg aat gaa tgg aaa cta aac atg aat aaa tac gat . 1680  
 Phe Tyr His Ile Leu Asn Glu Trp Lys Leu Asn Met Asn Lys Tyr Asp  
 545 550 555 560

aaa ccg cat agt gcc caa ttc att cag tcc ttg att gac gat tac tgc 1728  
 Lys Pro His Ser Ala Gln Phe Ile Gln Ser Leu Ile Asp Asp Tyr Cys  
 565 570 575

ttg gtc aat att gtt gac aat gac tac att tct cca gat gat caa atc 1776  
 Leu Val Asn Ile Val Asp Asn Asp Tyr Ile Ser Pro Asp Asp Gln Ile  
 580 585 590

cat tcc atc cta cta agc cta taa 1800  
 His Ser Ile Leu Leu Ser Leu  
 595

<210> 24  
 <211> 599  
 <212> PRT  
 <213> *Saccharomyces cerevisiae*

<400> 24  
 Met Lys Ile Thr Glu Lys Leu Glu Gln His Arg Gln Thr Ser Gly Lys  
 1 5 10 15

Pro Thr Tyr Ser Phe Glu Tyr Phe Val Pro Lys Thr Thr Gln Gly Val  
 20 25 30

Gln Asn Leu Tyr Asp Arg Met Asp Arg Met Tyr Glu Ala Ser Leu Pro  
 35 40 45

Gln Phe Ile Asp Ile Thr Trp Asn Ala Gly Gly Arg Leu Ser His  
 50 55 60

Leu Ser Thr Asp Leu Val Ala Thr Ala Gln Ser Val Leu Gly Leu Glu  
 65 70 75 80

Thr Cys Met His Leu Thr Cys Thr Asn Met Pro Ile Ser Met Ile Asp  
 85 90 95

Asp Ala Leu Glu Asn Ala Tyr His Ser Gly Cys Gln Asn Ile Leu Ala  
 100 105 110

Leu Arg Gly Asp Pro Pro Arg Asp Ala Glu Asn Trp Thr Pro Val Glu  
 115 120 125

Gly Gly Phe Gln Tyr Ala Lys Asp Leu Ile Lys Tyr Ile Lys Ser Lys  
 130 135 140

Tyr Gly Asp His Phe Ala Ile Gly Val Ala Gly Tyr Pro Glu Cys His  
 145 150 155 160

Pro Glu Leu Pro Asn Lys Asp Val Lys Leu Asp Leu Glu Tyr Leu Ser  
 165 170 175

Arg Arg Ser Thr Gly Gly Asp Phe Ile Ile Thr Gln Met Phe Tyr Asp

180	185	190
Val Asp Asn Leu Leu Asn Trp Cys Ser Gln Val Arg Ala Ala Gly Met		
195	200	205
Asp Val Pro Ile Ile Pro Gly Ile Met Pro Ile Thr Thr Tyr Ala Ala		
210	215	220
Phe Leu Arg Arg Ile Gln Trp Gly Gln Ile Ser Ile Pro Gln His Phe		
225	230	235
Ser Ser Arg Leu Asp Pro Ile Lys Asp Asp Asp Glu Leu Val Arg Asp		
245	250	255
Ile Gly Thr Asn Leu Ile Val Glu Met Cys Gln Lys Leu Leu Asp Ser		
260	265	270
Gly Tyr Val Ser His Leu His Ile Tyr Thr Met Asn Leu Glu Lys Ala		
275	280	285
Pro Leu Met Ile Leu Glu Arg Leu Asn Ile Leu Pro Thr Glu Ser Glu		
290	295	300
Phe Asn Ala His Pro Leu Ala Val Leu Pro Trp Arg Lys Ser Leu Asn		
305	310	315
320		
Pro Lys Arg Lys Asn Glu Glu Val Arg Pro Ile Phe Trp Lys Arg Arg		
325	330	335
Pro Tyr Ser Tyr Val Ala Arg Thr Ser Gln Trp Ala Val Asp Glu Phe		
340	345	350
Pro Asn Gly Arg Phe Gly Asp Ser Ser Ser Pro Ala Phe Gly Asp Leu		
355	360	365
Asp Leu Cys Gly Ser Asp Leu Ile Arg Gln Ser Ala Asn Lys Cys Leu		
370	375	380
Glu Leu Trp Ser Thr Pro Thr Ser Ile Asn Asp Val Ala Phe Leu Val		
385	390	395
400		
Ile Asn Tyr Leu Asn Gly Asn Leu Lys Cys Leu Pro Trp Ser Asp Ile		
405	410	415
Pro Ile Asn Asp Glu Ile Asn Pro Ile Lys Ala His Leu Ile Glu Leu		
420	425	430
Asn Gln His Ser Ile Ile Thr Ile Asn Ser Gln Pro Gln Val Asn Gly		
435	440	445
Ile Arg Ser Asn Asp Lys Ile His Gly Trp Gly Pro Lys Asp Gly Tyr		
450	455	460
Val Tyr Gln Lys Gln Tyr Leu Glu Phe Met Leu Pro Lys Thr Lys Leu		
465	470	475
480		
Pro Lys Leu Ile Asp Thr Leu Lys Asn Asn Glu Phe Leu Thr Tyr Phe		
485	490	495
Ala Ile Asp Ser Gln Gly Asp Leu Leu Ser Asn His Pro Asp Asn Ser		

500

505

510

Lys Ser Asn Ala Val Thr Trp Gly Ile Phe Pro Gly Arg Glu Ile Leu  
 515 520 525

Gln Pro Thr Ile Val Glu Lys Ile Ser Phe Leu Ala Trp Lys Glu Glu  
 530 535 540

Phe Tyr His Ile Leu Asn Glu Trp Lys Leu Asn Met Asn Lys Tyr Asp  
 545 550 555 560

Lys Pro His Ser Ala Gln Phe Ile Gln Ser Leu Ile Asp Asp Tyr Cys  
 565 570 575

Leu Val Asn Ile Val Asp Asn Asp Tyr Ile Ser Pro Asp Asp Gln Ile  
 580 585 590

His Ser Ile Leu Leu Ser Leu  
 595

&lt;210&gt; 25

&lt;211&gt; 897

&lt;212&gt; DNA

&lt;213&gt; Erwinia carotovora

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(894)

&lt;223&gt; RE000089

&lt;400&gt; 25

atg agc ttt ttt cac gca aac cag cg<sup>g</sup> gaa g<sup>c</sup> g<sup>c</sup> ctg aat caa agt ctg 48  
 Met Ser Phe Phe His Ala Asn Gln Arg Glu Ala Leu Asn Gln Ser Leu  
 1 5 10 15

g<sup>c</sup> g<sup>g</sup> gaa ttg c<sup>a</sup> g g<sup>g</sup> a c<sup>g</sup> a att aat gtg tca ttt gaa ttt ttc cc<sup>g</sup> cc<sup>a</sup> 96  
 Ala Glu Leu Gln Gly Arg Ile Asn Val Ser Phe Glu Phe Phe Pro Pro  
 20 25 30

cgt acc agc gat atg gaa gaa acc ctg tgg agc tct atc gat cga ctg 144  
 Arg Thr Ser Asp Met Glu Glu Thr Leu Trp Ser Ser Ile Asp Arg Leu  
 35 40 45

agc agc ctg aag ccc aag ttt gtt tcc gtg act tac ggg g<sup>c</sup> g<sup>c</sup> aat tct 192  
 Ser Ser Leu Lys Pro Lys Phe Val Ser Val Thr Tyr Gly Ala Asn Ser  
 50 55 60

ggc gag cgt gac cgt act cac agc att atc aaa acg att aaa gag cgt 240  
 Gly Glu Arg Asp Arg Thr His Ser Ile Ile Lys Thr Ile Lys Glu Arg  
 65 70 75 80

acc ggt ctg gaa g<sup>c</sup> g<sup>c</sup> g<sup>c</sup> cct cac ctg acc tgc atc gat gct tca cgc 288  
 Thr Gly Leu Glu Ala Ala Pro His Leu Thr Cys Ile Asp Ala Ser Arg  
 85 90 95

gaa cag ctg cgt gaa atc gct cag gat tac tgg gag agt ggt atc cgc 336  
 Glu Gln Leu Arg Glu Ile Ala Gln Asp Tyr Trp Glu Ser Gly Ile Arg  
 100 105 110

cat att gtc gcg ctg cgc ggc gac ttg cct caa gaa ggc ggc aaa ccg	384	
His Ile Val Ala Leu Arg Gly Asp Leu Pro Gln Glu Gly Gly Lys Pro		
115 120 125		
gac atg tac gcg gcg gat ctg gtt tcc ctg ctg aaa gag gtc ggt gat	432	
Asp Met Tyr Ala Ala Asp Leu Val Ser Leu Leu Lys Glu Val Gly Asp		
130 135 140		
ttc gat att tcc gtt gcc gcc tat cct gaa gta cac cct gaa gcg aaa	480	
Phe Asp Ile Ser Val Ala Ala Tyr Pro Glu Val His Pro Glu Ala Lys		
145 150 155 160		
agc gcg cag gct gac ctg att aac ctg aaa cac aag att gat gcc ggc	528	
Ser Ala Gln Ala Asp Leu Ile Asn Leu Lys His Lys Ile Asp Ala Gly		
165 170 175		
gcg aat cgc gct atc aca cag ttc ttt ttc gac gta gaa agc tat ttg	576	
Ala Asn Arg Ala Ile Thr Gln Phe Phe Asp Val Glu Ser Tyr Leu		
180 185 190		
cgg ttc cgt gac cgc tgc gtg gca acg ggc atc gat gta gaa att gtg	624	
Arg Phe Arg Asp Arg Cys Val Ala Thr Gly Ile Asp Val Glu Ile Val		
195 200 205		
ccg ggc att ctg cca gta tcg aac ttc aaa cag ttg cag aaa ttt gcc	672	
Pro Gly Ile Leu Pro Val Ser Asn Phe Lys Gln Leu Gln Lys Phe Ala		
210 215 220		
acg atg acc aac gtc cgt gtg ccg aac tgg atg acg acc atg ttt gac	720	
Thr Met Thr Asn Val Arg Val Pro Asn Trp Met Thr Thr Met Phe Asp		
225 230 235 240		
ggc ctg gat aac gat cca gaa acc cgc aaa atg gtg ggg gcg tct atc	768	
Gly Leu Asp Asn Asp Pro Glu Thr Arg Lys Met Val Gly Ala Ser Ile		
245 250 255		
gcc atg gat atg gtg aaa att ctc agc cgc gaa ggc gta aaa gat ttc	816	
Ala Met Asp Met Val Lys Ile Leu Ser Arg Glu Gly Val Lys Asp Phe		
260 265 270		
cat ttc tat acg ctg aac cgc gcg gag ctg agc tat gcg att tgc cat	864	
His Phe Tyr Thr Leu Asn Arg Ala Glu Leu Ser Tyr Ala Ile Cys His		
275 280 285		
acg ctg ggc gtc cgc cct gat gta gca cgc tga	897	
Thr Leu Gly Val Arg Pro Asp Val Ala Arg		
290 295		
<210> 26		
<211> 298		
<212> PRT		
<213> Erwinia carotovora		
<400> 26		
Met Ser Phe Phe His Ala Asn Gln Arg Glu Ala Leu Asn Gln Ser Leu		
1 5 10 15		
Ala Glu Leu Gln Gly Arg Ile Asn Val Ser Phe Glu Phe Phe Pro Pro		
20 25 30		

Arg Thr Ser Asp Met Glu Glu Thr Leu Trp Ser Ser Ile Asp Arg Leu  
 35 40 45  
 Ser Ser Leu Lys Pro Lys Phe Val Ser Val Thr Tyr Gly Ala Asn Ser  
 50 55 60  
 Gly Glu Arg Asp Arg Thr His Ser Ile Ile Lys Thr Ile Lys Glu Arg  
 65 70 75 80  
 Thr Gly Leu Glu Ala Ala Pro His Leu Thr Cys Ile Asp Ala Ser Arg  
 85 90 95  
 Glu Gln Leu Arg Glu Ile Ala Gln Asp Tyr Trp Glu Ser Gly Ile Arg  
 100 105 110  
 His Ile Val Ala Leu Arg Gly Asp Leu Pro Gln Glu Gly Gly Lys Pro  
 115 120 125  
 Asp Met Tyr Ala Ala Asp Leu Val Ser Leu Leu Lys Glu Val Gly Asp  
 130 135 140  
 Phe Asp Ile Ser Val Ala Ala Tyr Pro Glu Val His Pro Glu Ala Lys  
 145 150 155 160  
 Ser Ala Gln Ala Asp Leu Ile Asn Leu Lys His Lys Ile Asp Ala Gly  
 165 170 175  
 Ala Asn Arg Ala Ile Thr Gln Phe Phe Asp Val Glu Ser Tyr Leu  
 180 185 190  
 Arg Phe Arg Asp Arg Cys Val Ala Thr Gly Ile Asp Val Glu Ile Val  
 195 200 205  
 Pro Gly Ile Leu Pro Val Ser Asn Phe Lys Gln Leu Gln Lys Phe Ala  
 210 215 220  
 Thr Met Thr Asn Val Arg Val Pro Asn Trp Met Thr Thr Met Phe Asp  
 225 230 235 240  
 Gly Leu Asp Asn Asp Pro Glu Thr Arg Lys Met Val Gly Ala Ser Ile  
 245 250 255  
 Ala Met Asp Met Val Lys Ile Leu Ser Arg Glu Gly Val Lys Asp Phe  
 260 265 270  
 His Phe Tyr Thr Leu Asn Arg Ala Glu Leu Ser Tyr Ala Ile Cys His  
 275 280 285  
 Thr Leu Gly Val Arg Pro Asp Val Ala Arg  
 290 295

<210> 27  
 <211> 888  
 <212> DNA  
 <213> Klebsiella pneumoniae  
  
 <220>  
 <221> CDS

&lt;222&gt; (1)..(885)

&lt;223&gt; RKP07488

&lt;400&gt; 27

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 Met Ser Phe Phe His Ala Asn Gln Arg Glu Ala Leu Asn Gln Ser Leu  
 1 5 10 15

gct gaa gtc cag ggc cag att aat gtg tct ttt gaa ttc ttt ccg ccg 96  
 Ala Glu Val Gln Gly Gln Ile Asn Val Ser Phe Glu Phe Phe Pro Pro  
 20 25 30

cgc acc agt gaa atg gag caa acc ctg tgg aaa tcc atc gat cgc ctg 144  
 Arg Thr Ser Glu Met Glu Gln Thr Leu Trp Lys Ser Ile Asp Arg Leu  
 35 40 45

agc agt ctg aaa ccg aag ttt gtt tcg gta acc tat ggc gct aac tct 192  
 Ser Ser Leu Lys Pro Lys Phe Val Ser Val Thr Tyr Gly Ala Asn Ser  
 50 55 60

ggc gag cgc gat cgc acc cac agc atc atc aaa ggc att aaa gag cga 240  
 Gly Glu Arg Asp Arg Thr His Ser Ile Ile Lys Gly Ile Lys Glu Arg  
 65 70 75 80

acc ggt ctg gaa gca gct ccg cac ctg acc tgt atc gat gcc agc cgc 288  
 Thr Gly Leu Glu Ala Ala Pro His Leu Thr Cys Ile Asp Ala Ser Arg  
 85 90 95

gat gag ttg cgc act atc gct cag gat tac tgg aac aac ggt atc cgc 336  
 Asp Glu Leu Arg Thr Ile Ala Gln Asp Tyr Trp Asn Asn Gly Ile Arg  
 100 105 110

cat atc gtc gcc ctg cgc ggc gac ctg ccg ccg ggc agc ggt aaa ccg 384  
 His Ile Val Ala Leu Arg Gly Asp Leu Pro Pro Gly Ser Gly Lys Pro  
 115 120 125

gat atg tac gcc gct gat ctg gtg acg ttg ctg aaa gag gta ggc gat 432  
 Asp Met Tyr Ala Ala Asp Leu Val Thr Leu Leu Lys Glu Val Gly Asp  
 130 135 140

ttt gat atc tct gtc gcc gct tat ccg gaa gtg cat ccg gag gct aaa 480  
 Phe Asp Ile Ser Val Ala Ala Tyr Pro Glu Val His Pro Glu Ala Lys  
 145 150 155 160

agc gct cag gct gat tta ctg aac ctg aag cgc aaa gta gaa gca ggg 528  
 Ser Ala Gln Ala Asp Leu Leu Asn Leu Lys Arg Lys Val Glu Ala Gly  
 165 170 175

gcc aac cgc gct atc acc cag ttc ttc gat gtg gaa agc tac ctg 576  
 Ala Asn Arg Ala Ile Thr Gln Phe Phe Asp Val Glu Ser Tyr Leu  
 180 185 190

cgt ttt cgc gat cgc tgc gtc tcg gca ggc atc gac gtg gaa atc att 624  
 Arg Phe Arg Asp Arg Cys Val Ser Ala Gly Ile Asp Val Glu Ile Ile  
 195 200 205

ccc ggt atc ctg ccg gtc tcc aac ttt aaa cag gct aaa aag ttt gct 672  
 Pro Gly Ile Leu Pro Val Ser Asn Phe Lys Gln Ala Lys Lys Phe Ala  
 210 215 220

gat atg acc aac gtc cgt atc ccg gtg tgg atg tca aaa atg ttc gaa	720
Asp Met Thr Asn Val Arg Ile Pro Val Trp Met Ser Lys Met Phe Glu	
225 230 235 240	
ggg ctg gat aac gac gcc gaa acc cgt caa ctg gtg ggg gcg aat atc	768
Gly Leu Asp Asn Asp Ala Glu Thr Arg Gln Leu Val Gly Ala Asn Ile	
245 250 255	
gcc atg gac atg gtg aag atc tta agc ccg gaa ggg gtc aag gat ttc	816
Ala Met Asp Met Val Lys Ile Leu Ser Arg Glu Gly Val Lys Asp Phe	
260 265 270	
cac ttc tac acc ctg aac cgc gcc gag atg agc tac gcc atc tgc cat	864
His Phe Tyr Thr Leu Asn Arg Ala Glu Met Ser Tyr Ala Ile Cys His	
275 280 285	
acg ctg ggc gta cgc ccg gcc tga	888
Thr Leu Gly Val Arg Pro Ala	
290 295	

<210> 28  
 <211> 295  
 <212> PRT  
 <213> Klebsiella pneumoniae

<400> 28	
Met Ser Phe Phe His Ala Asn Gln Arg Glu Ala Leu Asn Gln Ser Leu	
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Arg Thr Ser Glu Met Glu Gln Thr Leu Trp Lys Ser Ile Asp Arg Leu	
35 40 45	
Ser Ser Leu Lys Pro Lys Phe Val Ser Val Thr Tyr Gly Ala Asn Ser	
50 55 60	
Gly Glu Arg Asp Arg Thr His Ser Ile Ile Lys Gly Ile Lys Glu Arg	
65 70 75 80	
Thr Gly Leu Glu Ala Ala Pro His Leu Thr Cys Ile Asp Ala Ser Arg	
85 90 95	
Asp Glu Leu Arg Thr Ile Ala Gln Asp Tyr Trp Asn Asn Gly Ile Arg	
100 105 110	
His Ile Val Ala Leu Arg Gly Asp Leu Pro Pro Gly Ser Gly Lys Pro	
115 120 125	
Asp Met Tyr Ala Ala Asp Leu Val Thr Leu Leu Lys Glu Val Gly Asp	
130 135 140	
Phe Asp Ile Ser Val Ala Ala Tyr Pro Glu Val His Pro Glu Ala Lys	
145 150 155 160	
Ser Ala Gln Ala Asp Leu Leu Asn Leu Lys Arg Lys Val Glu Ala Gly	
165 170 175	

Ala Asn Arg Ala Ile Thr Gln Phe Phe Asp Val Glu Ser Tyr Leu  
 180 185 190

Arg Phe Arg Asp Arg Cys Val Ser Ala Gly Ile Asp Val Glu Ile Ile  
 195 200 205

Pro Gly Ile Leu Pro Val Ser Asn Phe Lys Gln Ala Lys Lys Phe Ala  
 210 215 220

Asp Met Thr Asn Val Arg Ile Pro Val Trp Met Ser Lys Met Phe Glu  
 225 230 235 240

Gly Leu Asp Asn Asp Ala Glu Thr Arg Gln Leu Val Gly Ala Asn Ile  
 245 250 255

Ala Met Asp Met Val Lys Ile Leu Ser Arg Glu Gly Val Lys Asp Phe  
 260 265 270

His Phe Tyr Thr Leu Asn Arg Ala Glu Met Ser Tyr Ala Ile Cys His  
 275 280 285

Thr Leu Gly Val Arg Pro Ala  
 290 295

<210> 29

<211> 891

<212> DNA

<213> *Salmonella typhi*

<220>

<221> CDS

<222> (1)...(888)

<223> RTY02485

<400> 29

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 Met Ser Phe Phe His Ala Asn Gln Arg Glu Ala Leu Asn Gln Ser Leu  
 1 5 10 15

gc<sup>g</sup> gaa gta cag ggt cag att aac gtt tcg ttt gaa ttt ttc ccg ccg 96  
 Ala Glu Val Gln Gly Gln Ile Asn Val Ser Phe Glu Phe Pro Pro  
 20 25 30

cgc acc agt gaa atg gag caa acc ctg tgg aac tcc atc gat cgc ctg 144  
 Arg Thr Ser Glu Met Glu Gln Thr Leu Trp Asn Ser Ile Asp Arg Leu  
 35 40 45

agc agc ctg aaa ccg aag ttt gtt tcg gta acg tat ggc gcc aac tcc 192  
 Ser Ser Leu Lys Pro Lys Phe Val Ser Val Thr Tyr Gly Ala Asn Ser  
 50 55 60

ggg gaa cgt gac cgc act cat agt gtt att aaa ggc att aaa gag cgt 240  
 Gly Glu Arg Asp Arg Thr His Ser Val Ile Lys Gly Ile Lys Glu Arg  
 65 70 75 80

act ggg ctt gag gcc gcg ccg cac ctt acc tgt att gac gcc acg cgc 288  
 Thr Gly Leu Glu Ala Ala Pro His Leu Thr Cys Ile Asp Ala Thr Arg  
 85 90 95

gat gaa ctg cgc acc atc gcc cgc gac tac tgg aat aac ggt atc cgc	336
Asp Glu Leu Arg Thr Ile Ala Arg Asp Tyr Trp Asn Asn Gly Ile Arg	
100 105 110	
cac att gtt gct ttg cgc ggc gat ttg ccg ccg ggc agc ggt aag ccg	384
His Ile Val Ala Leu Arg Gly Asp Leu Pro Pro Gly Ser Gly Lys Pro	
115 120 125	
gag atg tac gcc gcc gat ctg gtt ggt ttg ctc aaa gag gtg gtc gat	432
Glu Met Tyr Ala Ala Asp Leu Val Gly Leu Leu Lys Glu Val Val Asp	
130 135 140	
ttc gat att tca gta gcg gcc tat ccg gag gta cat ccg gaa gcg aaa	480
Phe Asp Ile Ser Val Ala Ala Tyr Pro Glu Val His Pro Glu Ala Lys	
145 150 155 160	
agc gcg cag gcc gat ctg ctt aat ctg aag cgt aaa gtg gat gct ggc	528
Ser Ala Gln Ala Asp Leu Leu Asn Leu Lys Arg Lys Val Asp Ala Gly	
165 170 175	
gct aac cgc gcg ata acc caa ttt ttc ttc gat gtg gaa agc tat ctg	576
Ala Asn Arg Ala Ile Thr Gln Phe Phe Asp Val Glu Ser Tyr Leu	
180 185 190	
cgt ttt cgc gac cgc tgt gtt tcc gcc ggt atc gac gta gaa att att	624
Arg Phe Arg Asp Arg Cys Val Ser Ala Gly Ile Asp Val Glu Ile Ile	
195 200 205	
ccc ggc att tta ccg gtg tct aac ttt aaa cag gcg aaa aaa ttt gcc	672
Pro Gly Ile Leu Pro Val Ser Asn Phe Lys Gln Ala Lys Lys Phe Ala	
210 215 220	
gat atg acc aat gtc cgc att ccg tcc tgg atg tcg ctg atg ttt gag	720
Asp Met Thr Asn Val Arg Ile Pro Ser Trp Met Ser Leu Met Phe Glu	
225 230 235 240	
ggg ctg gat gat gac gca gaa acc cgc aag ctg gtg ggc gct aac att	768
Gly Leu Asp Asp Asp Ala Glu Thr Arg Lys Leu Val Gly Ala Asn Ile	
245 250 255	
gcg atg gac atg gtg aaa att tta agc cgc gaa gga gtg aag gat ttc	816
Ala Met Asp Met Val Lys Ile Leu Ser Arg Glu Gly Val Lys Asp Phe	
260 265 270	
cac ttc tac acg ttg aat cgt gcg gaa atg agt tat gcc att tgc cac	864
His Phe Tyr Thr Leu Asn Arg Ala Glu Met Ser Tyr Ala Ile Cys His	
275 280 285	
acg ctg ggc gta aga ccg ggt tta taa	891
Thr Leu Gly Val Arg Pro Gly Leu	
290 295	

&lt;210&gt; 30

&lt;211&gt; 296

&lt;212&gt; PRT

<213> *Salmonella typhi*

&lt;400&gt; 30

Met Ser Phe Phe His Ala Asn Gln Arg Glu Ala Leu Asn Gln Ser Leu

1

5

10

15

Ala Glu Val Gln Gly Gln Ile Asn Val Ser Phe Glu Phe Phe Pro Pro  
 20 25 30

Arg Thr Ser Glu Met Glu Gln Thr Leu Trp Asn Ser Ile Asp Arg Leu  
 35 40 45

Ser Ser Leu Lys Pro Lys Phe Val Ser Val Thr Tyr Gly Ala Asn Ser  
 50 55 60

Gly Glu Arg Asp Arg Thr His Ser Val Ile Lys Gly Ile Lys Glu Arg  
 65 70 75 80

Thr Gly Leu Glu Ala Ala Pro His Leu Thr Cys Ile Asp Ala Thr Arg  
 85 90 95

Asp Glu Leu Arg Thr Ile Ala Arg Asp Tyr Trp Asn Asn Gly Ile Arg  
 100 105 110

His Ile Val Ala Leu Arg Gly Asp Leu Pro Pro Gly Ser Gly Lys Pro  
 115 120 125

Glu Met Tyr Ala Ala Asp Leu Val Gly Leu Leu Lys Glu Val Val Asp  
 130 135 140

Phe Asp Ile Ser Val Ala Ala Tyr Pro Glu Val His Pro Glu Ala Lys  
 145 150 155 160

Ser Ala Gln Ala Asp Leu Leu Asn Leu Lys Arg Lys Val Asp Ala Gly  
 165 170 175

Ala Asn Arg Ala Ile Thr Gln Phe Phe Asp Val Glu Ser Tyr Leu  
 180 185 190

Arg Phe Arg Asp Arg Cys Val Ser Ala Gly Ile Asp Val Glu Ile Ile  
 195 200 205

Pro Gly Ile Leu Pro Val Ser Asn Phe Lys Gln Ala Lys Lys Phe Ala  
 210 215 220

Asp Met Thr Asn Val Arg Ile Pro Ser Trp Met Ser Leu Met Phe Glu  
 225 230 235 240

Gly Leu Asp Asp Asp Ala Glu Thr Arg Lys Leu Val Gly Ala Asn Ile  
 245 250 255

Ala Met Asp Met Val Lys Ile Leu Ser Arg Glu Gly Val Lys Asp Phe  
 260 265 270

His Phe Tyr Thr Leu Asn Arg Ala Glu Met Ser Tyr Ala Ile Cys His  
 275 280 285

Thr Leu Gly Val Arg Pro Gly Leu  
 290 295

&lt;210&gt; 31

&lt;211&gt; 891

&lt;212&gt; DNA

<213> *Salmonella typhimurium*

<220>  
 <221> CDS  
 <222> (1)..(888)  
 <223> RSY00593

<400> 31

atg	agc	ttt	ttt	cac	gcc	aac	cag	cg	gaa	gcc	ctg	aat	cag	agc	ctg	48
Met	Ser	Phe	Phe	His	Ala	Asn	Gln	Arg	Glu	Ala	Leu	Asn	Gln	Ser	Leu	
1		5								10				15		

gcg

gaa	gta	cag	ggt	cag	att	aac	gtt	tcg	ttt	gaa	ttt	ttc	ccg	ccg	96
Ala	Glu	Val	Gln	Gly	Gln	Ile	Asn	Val	Ser	Phe	Glu	Phe	Phe	Pro	Pro
20									25				30		

cgc

acc	agt	gaa	atg	gag	caa	acc	ctg	tgg	aac	tcc	atc	gat	cgc	ctg	144
Arg	Thr	Ser	Glu	Met	Glu	Gln	Thr	Leu	Trp	Asn	Ser	Ile	Asp	Arg	Leu
35									40			45			

agc

agt	ctg	aaa	ccg	aag	ttt	gtt	tcg	gta	acg	tat	ggc	gcc	aac	tcc	192
Ser	Ser	Leu	Lys	Pro	Lys	Phe	Val	Ser	Val	Thr	Tyr	Gly	Ala	Asn	Ser
50					55					60					

ggg

gaa	cgc	gac	cg	acc	cat	agc	gtt	att	aaa	ggc	atc	aaa	gag	cgt	240
Gly	Glu	Arg	Asp	Arg	Thr	His	Ser	Val	Ile	Lys	Gly	Ile	Lys	Glu	Arg
65									70		75		80		

act

ggg	ctt	gag	gcc	cg	cc	ac	ctt	acc	tgt	att	gac	gcc	ac	cg	288
Thr	Gly	Leu	Glu	Ala	Ala	Pro	His	Leu	Thr	Cys	Ile	Asp	Ala	Thr	Arg
85									90			95			

gat

gaa	ctg	cgc	acc	atc	gcc	cg	gac	ta	tgg	aat	aac	gg	atc	cg	336
Asp	Glu	Leu	Arg	Thr	Ile	Ala	Arg	Asp	Tyr	Trp	Asn	Asn	Gly	Ile	Arg
100									105			110			

cac

att	gtc	gct	ttg	cg	gg	gat	ttg	cc	cc	gg	ag	gg	aa	cc	384
His	Ile	Val	Ala	Leu	Arg	Gly	Asp	Leu	Pro	Pro	Gly	Ser	Gly	Lys	Pro
115									120			125			

gag

atg	ta	g	cc	g	cc	gat	ctg	gtt	gg	ct	aaa	gag	gt	cc	gat	432
Glu	Met	Tyr	Ala	Ala	Asp	Leu	Val	Gly	Leu	Leu	Lys	Glu	Val	Ala	Asp	
130									135			140				

ttc

gat	att	tca	gta	cg	gg	tat	cc	gag	gta	cat	cc	gaa	cg	aa	480
Phe	Asp	Ile	Ser	Val	Ala	Ala	Tyr	Pro	Glu	Val	His	Pro	Glu	Ala	Lys
145									150			155			160

agc

g	cg	g	cc	g	at	ct	tt	aa	ct	aa	gg	at	gt	cc	g	at	528
Ser	Ala	Gln	Ala	Asp	Leu	Leu	Asn	Leu	Lys	Arg	Lys	Val	Asp	Ala	Gly		
165									170			175					

gct

aa	cc	cc	cc	aa	cc	cc	tt	tt	cc	cc	gat	gt	cc	g	at	576
Ala	Asn	Arg	Ala	Ile	Thr	Gln	Phe	Phe	Asp	Val	Glu	Ser	Tyr	Leu		
180									185			190				

cgt

ttt	cc	g	cc	cc	tt	tt	cc	cc	gg	at	cc	g	aa	tt	tt	624
Arg	Phe	Arg	Asp	Arg	Cys	Val	Ser	Ala	Gly	Ile	Asp	Val	Glu	Ile	Ile	
195									200			205				

ccc ggc att tta ccg gtg tct aac ttt aaa cag gca aaa aaa ttt gcc	672	
Pro Gly Ile Leu Pro Val Ser Asn Phe Lys Gln Ala Lys Lys Phe Ala		
210 215 220		
gat atg acc aat gtc cgc att ccg tcc tgg atg tca ctg atg ttt gag	720	
Asp Met Thr Asn Val Arg Ile Pro Ser Trp Met Ser Leu Met Phe Glu		
225 230 235 240		
ggg ctg gat aat gac gca gaa acc cgc aag ctg gtg ggc gct aac att	768	
Gly Leu Asp Asn Asp Ala Glu Thr Arg Lys Leu Val Gly Ala Asn Ile		
245 250 255		
gcg atg gac atg gtg aaa att tta agc cgt gaa gga gtg aag gat ttc	816	
Ala Met Asp Met Val Lys Ile Leu Ser Arg Glu Gly Val Lys Asp Phe		
260 265 270		
cac ttc tac acg ttg aat cgt gcg gaa atg agt tat gcc att tgc cac	864	
His Phe Tyr Thr Leu Asn Arg Ala Glu Met Ser Tyr Ala Ile Cys His		
275 280 285		
acg ctg ggc gta aga ccg ggt tta taa	891	
Thr Leu Gly Val Arg Pro Gly Leu		
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<211> 296		
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<213> <i>Salmonella typhimurium</i>		
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Arg Thr Ser Glu Met Glu Gln Thr Leu Trp Asn Ser Ile Asp Arg Leu		
35 40 45		
Ser Ser Leu Lys Pro Lys Phe Val Ser Val Thr Tyr Gly Ala Asn Ser		
50 55 60		
Gly Glu Arg Asp Arg Thr His Ser Val Ile Lys Gly Ile Lys Glu Arg		
65 70 75 80		
Thr Gly Leu Glu Ala Ala Pro His Leu Thr Cys Ile Asp Ala Thr Arg		
85 90 95		
Asp Glu Leu Arg Thr Ile Ala Arg Asp Tyr Trp Asn Asn Gly Ile Arg		
100 105 110		
His Ile Val Ala Leu Arg Gly Asp Leu Pro Pro Gly Ser Gly Lys Pro		
115 120 125		
Glu Met Tyr Ala Ala Asp Leu Val Gly Leu Leu Lys Glu Val Ala Asp		
130 135 140		
Phe Asp Ile Ser Val Ala Ala Tyr Pro Glu Val His Pro Glu Ala Lys		
145 150 155 160		

Ser Ala Gln Ala Asp Leu Leu Asn Leu Lys Arg Lys Val Asp Ala Gly  
 165 170 175

Ala Asn Arg Ala Ile Thr Gln Phe Phe Asp Val Glu Ser Tyr Leu  
 180 185 190

Arg Phe Arg Asp Arg Cys Val Ser Ala Gly Ile Asp Val Glu Ile Ile  
 195 200 205

Pro Gly Ile Leu Pro Val Ser Asn Phe Lys Gln Ala Lys Lys Phe Ala  
 210 215 220

Asp Met Thr Asn Val Arg Ile Pro Ser Trp Met Ser Leu Met Phe Glu  
 225 230 235 240

Gly Leu Asp Asn Asp Ala Glu Thr Arg Lys Leu Val Gly Ala Asn Ile  
 245 250 255

Ala Met Asp Met Val Lys Ile Leu Ser Arg Glu Gly Val Lys Asp Phe  
 260 265 270

His Phe Tyr Thr Leu Asn Arg Ala Glu Met Ser Tyr Ala Ile Cys His  
 275 280 285

Thr Leu Gly Val Arg Pro Gly Leu  
 290 295

<210> 33

<211> 891

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)..(888)

<223> REC03839

<400> 33

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 1 5 10 15

gca gaa gtc cag ggg cag att aac gtt tcg ttc gag ttt ttc ccgtt ccgtt 96  
 Ala Glu Val Gln Gly Gln Ile Asn Val Ser Phe Glu Phe Pro Pro  
 20 25 30

cgt acc agt gaa atg gag cag acc ctgtt tgg aac tcc atc gat cgc ctt 144  
 Arg Thr Ser Glu Met Glu Gln Thr Leu Trp Asn Ser Ile Asp Arg Leu  
 35 40 45

agc agc ctgtt aaa ccgtt aag ttt gta tcg gtgtt acc tat ggc gctt aac tcc 192  
 Ser Ser Leu Lys Pro Lys Phe Val Ser Val Thr Tyr Gly Ala Asn Ser

50 55 60

ggc gag cgc gac cgt acg cac agc att att aaa ggc att aaa gat cgc 240  
 Gly Glu Arg Asp Arg Thr His Ser Ile Ile Lys Gly Ile Lys Asp Arg  
 65 70 75 80

act ggt ctg gaa gcg gca ccg cat ctt act tgc att gat gcg acg ccc	288
Thr Gly Leu Glu Ala Ala Pro His Leu Thr Cys Ile Asp Ala Thr Pro	
85 90 95	
gac gag ctg cgc acc att gca cgc gac tac tgg aat aac ggt att cgt	336
Asp Glu Leu Arg Thr Ile Ala Arg Asp Tyr Trp Asn Asn Gly Ile Arg	
100 105 110	
cat atc gtg gcg ctg cgt ggc gat ctg ccg gga agt ggt aag cca	384
His Ile Val Ala Leu Arg Gly Asp Leu Pro Pro Gly Ser Gly Lys Pro	
115 120 125	
gaa atg tat gct tct gac ctg gtg acg ctg tta aaa gaa gtg gca gat	432
Glu Met Tyr Ala Ser Asp Leu Val Thr Leu Leu Lys Glu Val Ala Asp	
130 135 140	
ttc gat atc tcc gtg gcg gcg tat ccg gaa gtt cac ccg gaa gca aaa	480
Phe Asp Ile Ser Val Ala Ala Tyr Pro Glu Val His Pro Glu Ala Lys	
145 150 155 160	
agc gct cag gcg gat ttg ctt aat ctg aaa cgc aaa gtg gat gcc gga	528
Ser Ala Gln Ala Asp Leu Leu Asn Leu Lys Arg Lys Val Asp Ala Gly	
165 170 175	
gcc aac cgc gcg att act cag ttc ttc gat gtc gaa agc tac ctg	576
Ala Asn Arg Ala Ile Thr Gln Phe Phe Asp Val Glu Ser Tyr Leu	
180 185 190	
cgt ttt cgt gac cgc tgt gta tcg gcg ggc att gat gtg gaa att att	624
Arg Phe Arg Asp Arg Cys Val Ser Ala Gly Ile Asp Val Glu Ile Ile	
195 200 205	
ccg gga att ttg ccg gta tct aac ttt aaa cag gcg aag aaa ttt gcc	672
Pro Gly Ile Leu Pro Val Ser Asn Phe Lys Gln Ala Lys Lys Phe Ala	
210 215 220	
gat atg acc aac gtg cgt att ccg gcg tgg atg gcg caa atg ttc gac	720
Asp Met Thr Asn Val Arg Ile Pro Ala Trp Met Ala Gln Met Phe Asp	
225 230 235 240	
ggt ctg gat gat gat gcc gaa acc cgc aaa ctg gtt ggc gcg aat att	768
Gly Leu Asp Asp Asp Ala Glu Thr Arg Lys Leu Val Gly Ala Asn Ile	
245 250 255	
gcc atg gat atg gtg aag att tta agc cgt gaa gga gtg aaa gat ttc	816
Ala Met Asp Met Val Lys Ile Leu Ser Arg Glu Gly Val Lys Asp Phe	
260 265 270	
cac ttc tat acg ctt aac cgt gct gaa atg agt tac gcg att tgc cat	864
His Phe Tyr Thr Leu Asn Arg Ala Glu Met Ser Tyr Ala Ile Cys His	
275 280 285	
acg ctg ggg gtt cga cct ggt tta taa	891
Thr Leu Gly Val Arg Pro Gly Leu	
290 295	

<212> PRT

<213> *Escherichia coli*

<400> 34

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Ala Glu Val Gln Gly Gln Ile Asn Val Ser Phe Glu Phe Phe Pro Pro  
20 25 30

Arg Thr Ser Glu Met Glu Gln Thr Leu Trp Asn Ser Ile Asp Arg Leu  
                  35                 40                 45

Ser Ser Leu Lys Pro Lys Phe Val Ser Val Thr Tyr Gly Ala Asn Ser  
50 55 60

Gly Glu Arg Asp Arg Thr His Ser Ile Ile Lys Gly Ile Lys Asp Arg  
65 70 75 80

Thr Gly Leu Glu Ala Ala Pro His Leu Thr Cys Ile Asp Ala Thr Pro  
85 90 95

Asp Glu Leu Arg Thr Ile Ala Arg Asp Tyr Trp Asn Asn Gly Ile Arg  
100 105 110

His Ile Val Ala Leu Arg Gly Asp Leu Pro Pro Gly Ser Gly Lys Pro  
115 120 125

Glu Met Tyr Ala Ser Asp Leu Val Thr Leu Leu Lys Glu Val Ala Asp  
 130 135 140

Phe Asp Ile Ser Val Ala Ala Tyr Pro Glu Val His Pro Glu Ala Lys  
145 150 155 160

Ser Ala Gln Ala Asp-Leu Leu Asn Leu Lys Arg Lys Val Asp Ala Gly  
                  165                 170                 175

Ala Asn Arg Ala Ile Thr Gln Phe Phe Phe Asp Val Glu Ser Tyr Leu  
180 185 190

Arg Phe Arg Asp Arg Cys Val Ser Ala Gly Ile Asp Val Glu Ile Ile  
195 200 205

Pro Gly Ile Leu Pro Val Ser Asn Phe Lys Gln Ala Lys Lys Phe Ala  
210 215 220

Asp	Met	Thr	Asn	Val	Arg	Ile	Pro	Ala	Trp	Met	Ala	Gln	Met	Phe	Asp
225				230						235					240

Gly Leu Asp Asp Asp Ala Glu Thr Arg Lys Leu Val Gly Ala Asn Ile  
245 250 255

Ala Met Asp Met Val Lys Ile Leu Ser Arg Glu Gly Val Lys Asp Phe  
260 265 270

His Phe Tyr Thr Leu Asn Arg Ala Glu Met Ser Tyr Ala Ile Cys His  
275 280 285

Thr Leu Gly Val Arg Pro Gly Leu  
290 295



ttc ttt gat gta gaa agc tac ctg cgt ttt cgc gat cgc tgt gtg gcc	624
Phe Phe Asp Val Glu Ser Tyr Leu Arg Phe Arg Asp Arg Cys Val Ala	
195 200 205	
gct ggg att gac gta gaa atc gtg cct ggc att ctg ccg gtt tct aac	672
Ala Gly Ile Asp Val Glu Ile Val Pro Gly Ile Leu Pro Val Ser Asn	
210 215 220	
ttt aaa caa gcg tcg cgc ttc gct gcg caa aac aac gtc aaa gtt ccg	720
Phe Lys Gln Ala Ser Arg Phe Ala Ala Gln Asn Asn Val Lys Val Pro	
225 230 235 240	
aat tgg atg gtg aag cag ttt gaa gga tta gaa gac gat cca gtg act	768
Asn Trp Met Val Lys Gln Phe Glu Gly Leu Glu Asp Asp Pro Val Thr	
245 250 255	
cgc cag ttg gta ggt gca agc caa gcc att gat atg gtg cgc gtg ctg	816
Arg Gln Leu Val Gly Ala Ser Gln Ala Ile Asp Met Val Arg Val Leu	
260 265 270	
tgc cgt gaa ggg gtg aag gat ttc cac ttc tac acc cta aat cgt gcc	864
Cys Arg Glu Gly Val Lys Asp Phe His Phe Tyr Thr Leu Asn Arg Ala	
275 280 285	
gaa atg act tac gcg tta tgc cac acc tta ggc gtt cgc cca caa gct	912
Glu Met Thr Tyr Ala Leu Cys His Thr Leu Gly Val Arg Pro Gln Ala	
290 295 300	
taa	915

<210> 36  
 <211> 304  
 <212> PRT  
 <213> Vibrio cholerae

<400> 36	
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His Ile Asp Ala Leu Asn Gln Asn Ile Ala Glu Leu Ser Asp Ile Asn	
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Val Ser Phe Glu Phe Phe Pro Pro Ser Ser Pro Gln Met Glu Glu Thr	
35 40 45	
Leu Trp Gly Ser Val His Arg Leu Lys Thr Leu Gln Pro Lys Phe Val	
50 55 60	
Ser Val Thr Tyr Gly Ala Asn Ser Gly Glu Arg Asp Arg Thr His Ser	
65 70 75 80	
Ile Ile Lys Ala Ile Lys Asp Gln Thr Gly Leu Ile Ala Ala Pro His	
85 90 95	
Leu Thr Cys Ile Asp Ala Thr Arg Asp Glu Leu Ile Gln Ile Ala Asp	
100 105 110	
Asp Tyr Trp His Asn Gly Ile Gln Asn Ile Val Ala Leu Arg Gly Asp	

115	120	125
Ile Pro Ala Gly Gly Lys Pro Glu Met Tyr Ala Ser Asp Leu Val		
130	135	140
Thr Leu Leu Lys Ser Arg His Asp Phe Asp Ile Ser Val Ala Ala Phe		
145	150	155
160		
Pro Glu Val His Pro Glu Ala Lys Ser Ala Gln Ala Asp Leu Leu Asn		
165	170	175
Leu Lys Arg Lys Val Asp Ala Gly Ala Asn Arg Ala Ile Thr Gln Phe		
180	185	190
Phe Phe Asp Val Glu Ser Tyr Leu Arg Phe Arg Asp Arg Cys Val Ala		
195	200	205
Ala Gly Ile Asp Val Glu Ile Val Pro Gly Ile Leu Pro Val Ser Asn		
210	215	220
Phe Lys Gln Ala Ser Arg Phe Ala Ala Gln Asn Asn Val Lys Val Pro		
225	230	235
240		
Asn Trp Met Val Lys Gln Phe Glu Gly Leu Glu Asp Asp Pro Val Thr		
245	250	255
Arg Gln Leu Val Gly Ala Ser Gln Ala Ile Asp Met Val Arg Val Leu		
260	265	270
Cys Arg Glu Gly Val Lys Asp Phe His Phe Tyr Thr Leu Asn Arg Ala		
275	280	285
Glu Met Thr Tyr Ala Leu Cys His Thr Leu Gly Val Arg Pro Gln Ala		
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<210> 37

<211> 879

<212> DNA

<213> *Haemophilus influenzae*

<220>

<221> CDS

<222> (1)...(876)

<223> RHI06620

<400> 37

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1		5					10						15			

ttt	aat	aaa	aaa	att	aat	gtc	tcc	ttt	gaa	ttt	ttt	cca	cct	aaa	aac	96
Phe	Asn	Lys	Lys	Ile	Asn	Val	Ser	Phe	Glu	Phe	Phe	Pro	Pro	Lys	Asn	
20				25								30				

gaa	aaa	atg	gaa	acc	ctt	cta	tgg	gat	tca	att	cat	cgt	tta	aaa	gta	144
Glu	Lys	Met	Glu	Thr	Leu	Leu	Trp	Asp	Ser	Ile	His	Arg	Leu	Lys	Val	

35

40

45

tta aag cct aaa ttt gtg tca gtc act tac ggt gca aat tcg gga gaa	192
Leu Lys Pro Lys Phe Val Ser Val Thr Tyr Gly Ala Asn Ser Gly Glu	
50 55 60	
cgt gac cgc act cac ggc att gtg aaa gcc att aaa caa gaa act ggc	240
Arg Asp Arg Thr His Gly Ile Val Lys Ala Ile Lys Gln Glu Thr Gly	
65 70 75 80	
tta gaa gcc gca cca cat tta act gga att gat gcc aca cct gaa gaa	288
Leu Glu Ala Ala Pro His Leu Thr Gly Ile Asp Ala Thr Pro Glu Glu	
85 90 95	
tta aaa caa att gcg aga gat tat tgg gat agt ggt att cgc cgt att	336
Leu Lys Gln Ile Ala Arg Asp Tyr Trp Asp Ser Gly Ile Arg Arg Ile	
100 105 110	
gtt gcg tta cgc ggt gac gaa cct aaa ggt tac gcg aaa aaa cca ttt	384
Val Ala Leu Arg Gly Asp Glu Pro Lys Gly Tyr Ala Lys Lys Pro Phe	
115 120 125	
tat gcg tca gat ctt gtg gaa tta ctc cgt tct gtc gct gat ttt gat	432
Tyr Ala Ser Asp Leu Val Glu Leu Leu Arg Ser Val Ala Asp Phe Asp	
130 135 140	
att tct gta gcc gct tat ccc gaa gtt cat cca gaa gca aaa tcc gca	480
Ile Ser Val Ala Ala Tyr Pro Glu Val His Pro Glu Ala Lys Ser Ala	
145 150 155 160	
caa gca gac tta att aat tta aaa cgt aaa att gat gca ggt gca aac	528
Gln Ala Asp Leu Ile Asn Leu Lys Arg Lys Ile Asp Ala Gly Ala Asn	
165 170 175	
cac gtc att aca caa ttt ttc ttt gat att gaa aac tac cta cgt ttt	576
His Val Ile Thr Gln Phe Phe Asp Ile Glu Asn Tyr Leu Arg Phe	
180 185 190	
cgt gat cgt tgt gca tca att ggt att gat act gaa atc gta ccc ggt	624
Arg Asp Arg Cys Ala Ser Ile Gly Ile Asp Thr Glu Ile Val Pro Gly	
195 200 205	
att tta cct gtt act aat ttt aaa caa ctc caa aaa atg gca tca ttc	672
Ile Leu Pro Val Thr Asn Phe Lys Gln Leu Gln Lys Met Ala Ser Phe	
210 215 220	
act aat gtg aaa att cca gcg tgg tta gtt aaa gcc tat gat ggt ttg	720
Thr Asn Val Lys Ile Pro Ala Trp Leu Val Lys Ala Tyr Asp Gly Leu	
225 230 235 240	
gat aat gat cca act aca cgt aat ctt gtg gca gca agt gtt gca atg	768
Asp Asn Asp Pro Thr Thr Arg Asn Leu Val Ala Ala Ser Val Ala Met	
245 250 255	
gat atg gta aaa att tta tct cgc gaa ggc gtg aat gac ttc cac ttt	816
Asp Met Val Lys Ile Leu Ser Arg Glu Gly Val Asn Asp Phe His Phe	
260 265 270	
tat aca tta aat cgt agt gaa tta act tat gct atc tgt cat atg tta	864
Tyr Thr Leu Asn Arg Ser Glu Leu Thr Tyr Ala Ile Cys His Met Leu	

275

280

285

ggt gta aga cct taa  
 Gly Val Arg Pro  
 290

879

<210> 38  
 <211> 292  
 <212> PRT  
 <213> Haemophilus influenzae

<400> 38  
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Phe Asn Lys Lys Ile Asn Val Ser Phe Glu Phe Phe Pro Pro Lys Asn  
 20 25 30

Glu Lys Met Glu Thr Leu Leu Trp Asp Ser Ile His Arg Leu Lys Val  
 35 40 45

Leu Lys Pro Lys Phe Val Ser Val Thr Tyr Gly Ala Asn Ser Gly Glu  
 50 55 60

Arg Asp Arg Thr His Gly Ile Val Lys Ala Ile Lys Gln Glu Thr Gly  
 65 70 75 80

Leu Glu Ala Ala Pro His Leu Thr Gly Ile Asp Ala Thr Pro Glu Glu  
 85 90 95

Leu Lys Gln Ile Ala Arg Asp Tyr Trp Asp Ser Gly Ile Arg Arg Ile  
 100 105 110

Val Ala Leu Arg Gly Asp Glu Pro Lys Gly Tyr Ala Lys Lys Pro Phe  
 115 120 125

Tyr Ala Ser Asp Leu Val Glu Leu Leu Arg Ser Val Ala Asp Phe Asp  
 130 135 140

Ile Ser Val Ala Ala Tyr Pro Glu Val His Pro Glu Ala Lys Ser Ala  
 145 150 155 160

Gln Ala Asp Leu Ile Asn Leu Lys Arg Lys Ile Asp Ala Gly Ala Asn  
 165 170 175

His Val Ile Thr Gln Phe Phe Asp Ile Glu Asn Tyr Leu Arg Phe  
 180 185 190

Arg Asp Arg Cys Ala Ser Ile Gly Ile Asp Thr Glu Ile Val Pro Gly  
 195 200 205

Ile Leu Pro Val Thr Asn Phe Lys Gln Leu Gln Lys Met Ala Ser Phe  
 210 215 220

Thr Asn Val Lys Ile Pro Ala Trp Leu Val Lys Ala Tyr Asp Gly Leu  
 225 230 235 240

Asp Asn Asp Pro Thr Thr Arg Asn Leu Val Ala Ala Ser Val Ala Met

245

250

255

Asp Met Val Lys Ile Leu Ser Arg Glu Gly Val Asn Asp Phe His Phe  
 260 265 270

Tyr Thr Leu Asn Arg Ser Glu Leu Thr Tyr Ala Ile Cys His Met Leu  
 275 280 285

Gly Val Arg Pro  
 290

<210> 39  
 <211> 945  
 <212> DNA  
 <213> Caulobacter crescentus

<220>  
 <221> CDS  
 <222> (1)..(942)  
 <223> RCO02274

<400> 39  
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ggc gag cgg acc ggc cgt ccg cgc gtg tcg ttc gag ttc ttc ccg ccc 96  
 Gly Glu Arg Thr Gly Arg Pro Arg Val Ser Phe Glu Phe Phe Pro Pro  
 20 25 30

aag act ccg cag atg gaa gag agc ctg tgg cag gcg atc aca cgc ctg 144  
 Lys Thr Pro Gln Met Glu Glu Ser Leu Trp Gln Ala Ile Thr Arg Leu  
 35 40 45

gcg ccg ctg gat ccg gcc ttc gtc tcg gtg acc tat ggc gcg ggc ggc 192  
 Ala Pro Leu Asp Pro Ala Phe Val Ser Val Thr Tyr Gly Ala Gly Gly  
 50 55 60

tcc acc cgc gag cgc acc cac cgc acc gtc aag cgg atc ctg gac gag 240  
 Ser Thr Arg Glu Arg Thr His Arg Thr Val Lys Arg Ile Leu Asp Glu  
 65 70 75 80

acc agc ctc aag ccc gcc gcg cac ctg acc tgc gtc ggc gcc agt cgc 288  
 Thr Ser Leu Lys Pro Ala Ala His Leu Thr Cys Val Gly Ala Ser Arg  
 85 90 95

gaa gag gtc gat gag gtc att cgc gag tac tgg gag acc ggg gtc cgt 336  
 Glu Glu Val Asp Glu Val Ile Arg Glu Tyr Trp Glu Thr Gly Val Arg  
 100 105 110

cac atc gtt tcg ctg cgg ggc gat ccg ccg ccc ggc gag ggc atc 384  
 His Ile Val Ser Leu Arg Gly Asp Pro Pro Gly Glu Gly Gly Ile  
 115 120 125

ggc ggg gtc tat gtg ccg cgc gcc gac ggc tac gcc aac gcc aca gag 432  
 Gly Gly Val Tyr Val Pro Arg Ala Asp Gly Tyr Ala Asn Ala Thr Glu  
 130 135 140

ttg acc aag gcc gtg cgc gcg atc gcg ccg ttc gag gtg ctg gtc ggg 480

Leu Thr Lys Ala Val Arg Ala Ile Ala Pro Phe Glu Val Leu Val Gly  
 145 150 155 160

gtc tat ccc gag aag cat ccc gag agc ccc tcg ttg gag cac gac atc 528  
 Val Tyr Pro Glu Lys His Pro Glu Ser Pro Ser Leu Glu His Asp Ile  
 165 170 175

gac gtc ttg aag cag aag gtc gac gcc ggc gcg acg ctg ggg atc agc 576  
 Asp Val Leu Lys Gln Lys Val Asp Ala Gly Ala Thr Leu Gly Ile Ser  
 180 185 190

cag ttc ttc ttc gac ctc gac gcc ttc ctg cgc ttc gtc gac aag gtg 624  
 Gln Phe Phe Asp Leu Asp Ala Phe Leu Arg Phe Val Asp Lys Val  
 195 200 205

cgc gcg ggc atc acc att ccg atc gtg ccg ggg atc atg ccg gtg 672  
 Arg Ala Ala Gly Ile Thr Ile Pro Ile Val Pro Gly Ile Met Pro Val  
 210 215 220

acc aat ttc gcg ggc ttg aag aag atg gcc gcc tgc cag acg gcc 720  
 Thr Asn Phe Ala Gly Leu Lys Lys Met Ala Ala Ala Cys Gln Thr Ala  
 225 230 235 240

atc ccg tcc tgg ctg ggg aac ctg ttc gac ggg ctg gag aac gac gcg 768  
 Ile Pro Ser Trp Leu Gly Asn Leu Phe Asp Gly Leu Glu Asn Asp Ala  
 245 250 255

gag acc cgc cgc ctg atc gcc tgt tcg gtg gcc gcc gag atg tgc gcc 816  
 Glu Thr Arg Arg Leu Ile Ala Cys Ser Val Ala Ala Glu Met Cys Ala  
 260 265 270

aag ctg cag gaa cag ggt ttc gag gac ttc cac ttc tac acc ctg aac 864  
 Lys Leu Gln Glu Gln Gly Phe Glu Asp Phe His Phe Tyr Thr Leu Asn  
 275 280 285

cgg gcc gat ctc gtt tac gcc atc tgc cgt gtg ctg ggc gtg cgc gag 912  
 Arg Ala Asp Leu Val Tyr Ala Ile Cys Arg Val Leu Gly Val Arg Glu  
 290 295 300

atc tcg ccc gcc gct tcg gag gtc gcc gca tga 945  
 Ile Ser Pro Ala Ala Ser Glu Val Ala Ala  
 305 310

<210> 40  
 <211> 314  
 <212> PRT  
 <213> Caulobacter crescentus

<400> 40  
 Met Thr Leu Pro Pro Thr Arg Arg Val Ile Gly Pro Val Ala Arg Ala  
 1 5 10 15

Gly Glu Arg Thr Gly Arg Pro Arg Val Ser Phe Glu Phe Phe Pro Pro  
 20 25 30

Lys Thr Pro Gln Met Glu Glu Ser Leu Trp Gln Ala Ile Thr Arg Leu  
 35 40 45

Ala Pro Leu Asp Pro Ala Phe Val Ser Val Thr Tyr Gly Ala Gly Gly

50

55

60

Ser Thr Arg Glu Arg Thr His Arg Thr Val Lys Arg Ile Leu Asp Glu  
 65                   70                   75                   80

Thr Ser Leu Lys Pro Ala Ala His Leu Thr Cys Val Gly Ala Ser Arg  
 85                   90                   95

Glu Glu Val Asp Glu Val Ile Arg Glu Tyr Trp Glu Thr Gly Val Arg  
 100                   105                   110

His Ile Val Ser Leu Arg Gly Asp Pro Pro Pro Gly Glu Gly Gly Ile  
 115                   120                   125

Gly Gly Val Tyr Val Pro Arg Ala Asp Gly Tyr Ala Asn Ala Thr Glu  
 130                   135                   140

Leu Thr Lys Ala Val Arg Ala Ile Ala Pro Phe Glu Val Leu Val Gly  
 145                   150                   155                   160

Val Tyr Pro Glu Lys His Pro Glu Ser Pro Ser Leu Glu His Asp Ile  
 165                   170                   175

Asp Val Leu Lys Gln Lys Val Asp Ala Gly Ala Thr Leu Gly Ile Ser  
 180                   185                   190

Gln Phe Phe Phe Asp Leu Asp Ala Phe Leu Arg Phe Val Asp Lys Val  
 195                   200                   205

Arg Ala Ala Gly Ile Thr Ile Pro Ile Val Pro Gly Ile Met Pro Val  
 210                   215                   220

Thr Asn Phe Ala Gly Leu Lys Lys Met Ala Ala Ala Cys Gln Thr Ala  
 225                   230                   235                   240

Ile Pro Ser Trp Leu Gly Asn Leu Phe Asp Gly Leu Glu Asn Asp Ala  
 245                   250                   255

Glu Thr Arg Arg Leu Ile Ala Cys Ser Val Ala Ala Glu Met Cys Ala  
 260                   265                   270

Lys Leu Gln Glu Gln Gly Phe Glu Asp Phe His Phe Tyr Thr Leu Asn  
 275                   280                   285

Arg Ala Asp Leu Val Tyr Ala Ile Cys Arg Val Leu Gly Val Arg Glu  
 290                   295                   300

Ile Ser Pro Ala Ala Ser Glu Val Ala Ala  
 305                   310

<210> 41  
 <211> 885  
 <212> DNA  
 <213> *Actinobacillus actinomycetemcomitans*

<220>  
 <221> CDS  
 <222> (1)..(882)

&lt;223&gt; RAB00260

<400> 41				
atg agt tac gca aaa gaa att gat aat cta aat caa cat tta gct gat	48			
Met Ser Tyr Ala Lys Glu Ile Asp Asn Leu Asn Gln His Leu Ala Asp				
1 5 10 15				
tta aac ggc aaa att aat gtc tct ttt gaa ttt ttc ccg ccg aaa agt	96			
Leu Asn Gly Lys Ile Asn Val Ser Phe Glu Phe Phe Pro Pro Lys Ser				
20 25 30				
gaa aaa atg gaa aat ctt ctg tgg gaa tcc atc cat cgc tta aaa gtg	144			
Glu Lys Met Glu Asn Leu Leu Trp Glu Ser Ile His Arg Leu Lys Val				
35 40 45				
cta aaa ccg aaa ttt gta tcc gtg act tac ggc gcc aat tcc ggc gag	192			
Leu Lys Pro Lys Phe Val Ser Val Thr Tyr Gly Ala Asn Ser Gly Glu				
50 55 60				
cgt gaa cgc act cac ggg gtg gtg aaa cgc att aag cag gaa acc ggt	240			
Arg Glu Arg Thr His Gly Val Val Lys Arg Ile Lys Gln Glu Thr Gly				
65 70 75 80				
ctg gaa gct gcg cat tta acc ggt att gac gct acc tcg gac gaa	288			
Leu Glu Ala Ala Pro His Leu Thr Gly Ile Asp Ala Thr Ser Asp Glu				
85 90 95				
ttg cgt cgc att gcc aaa ggt tat tgg gat agc ggc att cgt cgc att	336			
Leu Arg Arg Ile Ala Lys Gly Tyr Trp Asp Ser Gly Ile Arg Arg Ile				
100 105 110				
gtg gca ctg cgc ggt gac gag ccg aaa ggc tac gag aaa aaa cca ttt	384			
Val Ala Leu Arg Gly Asp Glu Pro Lys Gly Tyr Glu Lys Lys Pro Phe				
115 120 125				
tat gcc gcc gat tta gta gca tta cgt gac gta tca gat ttt gat	432			
Tyr Ala Ala Asp Leu Val Ala Leu Leu Arg Asp Val Ser Asp Phe Asp				
130 135 140				
att tcc gtg gcg gca tac cct gag gtt cat ccg gaa gcc aaa tcg gcg	480			
Ile Ser Val Ala Ala Tyr Pro Glu Val His Pro Glu Ala Lys Ser Ala				
145 150 155 160				
caa gcg gat tta att aat tta aaa cgt aaa att gat gcc ggt gcc aat	528			
Gln Ala Asp Leu Ile Asn Leu Lys Arg Lys Ile Asp Ala Gly Ala Asn				
165 170 175				
cat gtg atc aca caa ttc ttt ttc gat att gac agc tat ctg cgg ttc	576			
His Val Ile Thr Gln Phe Phe Asp Ile Asp Ser Tyr Leu Arg Phe				
180 185 190				
cgc gat cgc tgc gcg tct atc ggt att gat gca gaa atc gtg ccg ggg	624			
Arg Asp Arg Cys Ala Ser Ile Gly Ile Asp Ala Glu Ile Val Pro Gly				
195 200 205				
att ctg ccg gtg acc aac ttc aaa caa tta caa aaa atg gca gca atc	672			
Ile Leu Pro Val Thr Asn Phe Lys Gln Leu Gln Lys Met Ala Ala Ile				
210 215 220				
act aat gtg aaa att cca gct tgg atg agc aaa atg tat gaa ggc ttg	720			

Thr Asn Val Lys Ile Pro Ala Trp Met Ser Lys Met Tyr Glu Gly Leu  
 225 230 235 240

gat gat gac caa acc acc cgc aat ctg gtg gcg gcg agc atc gcc atg 768  
 Asp Asp Asp Gln Thr Thr Arg Asn Leu Val Ala Ala Ser Ile Ala Met  
 245 250 255

gac atg gtg cgt gta ctg tcc cgc gaa ggg gta aaa gac ttt cat ttc 816  
 Asp Met Val Arg Val Leu Ser Arg Glu Gly Val Lys Asp Phe His Phe  
 260 265 270

tac acc ctg aat cgc agt gaa ctc acc tat gct att tgc cac acg tta 864  
 Tyr Thr Leu Asn Arg Ser Glu Leu Thr Tyr Ala Ile Cys His Thr Leu  
 275 280 285

ggc att cgt ccg agt ttg taa 885  
 Gly Ile Arg Pro Ser Leu  
 290

<210> 42  
 <211> 294  
 <212> PRT  
 <213> *Actinobacillus actinomycetemcomitans*

<400> 42  
 Met Ser Tyr Ala Lys Glu Ile Asp Asn Leu Asn Gln His Leu Ala Asp  
 1 5 10 15

Leu Asn Gly Lys Ile Asn Val Ser Phe Glu Phe Phe Pro Pro Lys Ser  
 20 25 30

Glu Lys Met Glu Asn Leu Leu Trp Glu Ser Ile His Arg Leu Lys Val  
 35 40 45

Leu Lys Pro Lys Phe Val Ser Val Thr Tyr Gly Ala Asn Ser Gly Glu  
 50 55 60

Arg Glu Arg Thr His Gly Val Val Lys Arg Ile Lys Gln Glu Thr Gly  
 65 70 75 80

Leu Glu Ala Ala Pro His Leu Thr Gly Ile Asp Ala Thr Ser Asp Glu  
 85 90 95

Leu Arg Arg Ile Ala Lys Gly Tyr Trp Asp Ser Gly Ile Arg Arg Ile  
 100 105 110

Val Ala Leu Arg Gly Asp Glu Pro Lys Gly Tyr Glu Lys Lys Pro Phe  
 115 120 125

Tyr Ala Ala Asp Leu Val Ala Leu Leu Arg Asp Val Ser Asp Phe Asp  
 130 135 140

Ile Ser Val Ala Ala Tyr Pro Glu Val His Pro Glu Ala Lys Ser Ala  
 145 150 155 160

Gln Ala Asp Leu Ile Asn Leu Lys Arg Lys Ile Asp Ala Gly Ala Asn  
 165 170 175

His Val Ile Thr Gln Phe Phe Asp Ile Asp Ser Tyr Leu Arg Phe

180

185

190

Arg Asp Arg Cys Ala Ser Ile Gly Ile Asp Ala Glu Ile Val Pro Gly  
 195 200 205

Ile Leu Pro Val Thr Asn Phe Lys Gln Leu Gln Lys Met Ala Ala Ile  
 210 215 220

Thr Asn Val Lys Ile Pro Ala Trp Met Ser Lys Met Tyr Glu Gly Leu  
 225 230 235 240

Asp Asp Asp Gln Thr Thr Arg Asn Leu Val Ala Ala Ser Ile Ala Met  
 245 250 255

Asp Met Val Arg Val Leu Ser Arg Glu Gly Val Lys Asp Phe His Phe  
 260 265 270

Tyr Thr Leu Asn Arg Ser Glu Leu Thr Tyr Ala Ile Cys His Thr Leu  
 275 280 285

Gly Ile Arg Pro Ser Leu  
 290

&lt;210&gt; 43

&lt;211&gt; 867

&lt;212&gt; DNA

&lt;213&gt; Rhodobacter

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(864)

&lt;223&gt; RRC03981

&lt;400&gt; 43

atg acc acg ccg cat gtc agc ttt gaa ttc ttc ccg ccg cag acg ctc 48  
 Met Thr Thr Pro His Val Ser Phe Glu Phe Phe Pro Pro Gln Thr Leu  
 1 5 10 15

gac gcc tcg ttc ccg ctg tgg gag acg gcg cag gtt ctg gcg ccg ctc 96  
 Asp Ala Ser Phe Arg Leu Trp Glu Thr Ala Gln Val Leu Ala Pro Leu  
 20 25 30

aag ccc ggc ttc gtc tcg gtc acc tat ggc gcg ggc ggc acc acc cgc 144  
 Lys Pro Gly Phe Val Ser Val Thr Tyr Gly Ala Gly Gly Thr Thr Arg  
 35 40 45

aag ctg acg cat gag gcc gtg gcg atc cac aag aat tac ggc ctg 192  
 Lys Leu Thr His Glu Ala Val Ala Ala Ile His Lys Asn Tyr Gly Leu  
 50 55 60

aac gtc gcc gcg cat ctg acc tgc gtc gat gcg acc ccg gcc gaa acg 240  
 Asn Val Ala Ala His Leu Thr Cys Val Asp Ala Thr Arg Ala Glu Thr  
 65 70 75 80

caa gag atc atc gac gcc tat gcc gag gct ggc gtc acc gag att gtc 288  
 Gln Glu Ile Ile Asp Ala Tyr Ala Glu Ala Gly Val Thr Glu Ile Val  
 85 90 95

gcg ctg cgc ggt gat ccg ccg aaa ggc gcc gcc cgc ttc acg ccg cat 336

Ala Leu Arg Gly Asp Pro Pro Lys Gly Ala Ala Arg Phe Thr Pro His			
100	105	110	
ccg gac ggg ttt gcc tcc tcg gtg gac ctc atc gaa tgg ctg gcg cg			384
Pro Asp Gly Phe Ala Ser Ser Val Asp Leu Ile Glu Trp Leu Ala Arg			
115	120	125	
gac ggc cgc ttc acg ctg cgc tgc ggc gcc tat ccg gaa ccg cat ccg			432
Asp Gly Arg Phe Thr Leu Arg Cys Gly Ala Tyr Pro Glu Pro His Pro			
130	135	140	
gaa gcc gcc gac acg ctg gcc gac gtg cgc tgg ctg aaa cgc aaa tgc			480
Glu Ala Ala Asp Thr Leu Ala Asp Val Arg Trp Leu Lys Arg Lys Cys			
145	150	155	160
gag gcg ggg gcg acc tcg gcg atc acg caa ttc ttc ttt gaa gcc gag			528
Glu Ala Gly Ala Thr Ser Ala Ile Thr Gln Phe Phe Glu Ala Glu			
165	170	175	
acc ttc ttc cgc ttc cgc gac gcc tgc gtg aag gaa ggg atc acc acc gcc			576
Thr Phe Phe Arg Phe Arg Asp Ala Cys Val Lys Glu Gly Ile Thr Ala			
180	185	190	
aag atc atc ccg ggc atc ctg ccg atc cag tcc tgg aaa ggc gcc aag			624
Lys Ile Ile Pro Gly Ile Leu Pro Ile Gln Ser Trp Lys Gly Ala Lys			
195	200	205	
agc ttt gcg cag cgc tgc ggc acc tcg atc ccg acc tgg gtc gaa gag			672
Ser Phe Ala Gln Arg Cys Gly Thr Ser Ile Pro Thr Trp Val Glu Glu			
210	215	220	
gcc ttt gac cat gcg atc cgc gac cgc gaa cag ctg ctg gcc acg			720
Ala Phe Asp His Ala Ile Arg Asp Asp Arg Glu Gln Leu Leu Ala Thr			
225	230	235	240
gcg ctg tgc acg gag ctc tgc gac aac ctg atc gcg ggc ggg gtg gag			768
Ala Leu Cys Thr Glu Leu Cys Asp Asn Leu Ile Ala Gly Gly Val Glu			
245	250	255	
gat ctg cat ttc tac acg ctg aac cgg ccg cag atg acc ccg gat gtc			816
Asp Leu His Phe Tyr Thr Leu Asn Arg Pro Gln Met Thr Arg Asp Val			
260	265	270	
tgc cat gcg ctg ggc gtc aac ccg ggt gtg gtg ctg gaa aac gtc gcc			864
Cys His Ala Leu Gly Val Asn Pro Gly Val Val Leu Glu Asn Val Ala			
275	280	285	
tga			867

<210> 44  
 <211> 288  
 <212> PRT  
 <213> Rhodobacter

<400> 44  
 Met Thr Thr Pro His Val Ser Phe Glu Phe Phe Pro Pro Gln Thr Leu  
 1 5 10 15  
 Asp Ala Ser Phe Arg Leu Trp Glu Thr Ala Gln Val Leu Ala Pro Leu

20

25

30

Lys	Pro	Gly	Phe	Val	Ser	Val	Thr	Tyr	Gly	Ala	Gly	Gly	Thr	Thr	Arg
35							40						45		
Lys	Leu	Thr	His	Glu	Ala	Val	Ala	Ala	Ile	His	Lys	Asn	Tyr	Gly	Leu
50							55						60		
Asn	Val	Ala	Ala	His	Leu	Thr	Cys	Val	Asp	Ala	Thr	Arg	Ala	Glu	Thr
65							70				75			80	
Gln	Glu	Ile	Ile	Asp	Ala	Tyr	Ala	Glu	Ala	Gly	Val	Thr	Glu	Ile	Val
				85				90					95		
Ala	Leu	Arg	Gly	Asp	Pro	Pro	Lys	Gly	Ala	Ala	Arg	Phe	Thr	Pro	His
				100				105				110			
Pro	Asp	Gly	Phe	Ala	Ser	Ser	Val	Asp	Leu	Ile	Glu	Trp	Leu	Ala	Arg
				115				120				125			
Asp	Gly	Arg	Phe	Thr	Leu	Arg	Cys	Gly	Ala	Tyr	Pro	Glu	Pro	His	Pro
				130				135				140			
Glu	Ala	Ala	Asp	Thr	Leu	Ala	Asp	Val	Arg	Trp	Leu	Lys	Arg	Lys	Cys
				145				150				155			160
Glu	Ala	Gly	Ala	Thr	Ser	Ala	Ile	Thr	Gln	Phe	Phe	Glu	Ala	Glu	
				165				170				175			
Thr	Phe	Phe	Arg	Phe	Arg	Asp	Ala	Cys	Val	Lys	Glu	Gly	Ile	Thr	Ala
				180				185				190			
Lys	Ile	Ile	Pro	Gly	Ile	Leu	Pro	Ile	Gln	Ser	Trp	Lys	Gly	Ala	Lys
				195				200				205			
Ser	Phe	Ala	Gln	Arg	Cys	Gly	Thr	Ser	Ile	Pro	Thr	Trp	Val	Glu	Glu
				210				215				220			
Ala	Phe	Asp	His	Ala	Ile	Arg	Asp	Asp	Arg	Glu	Gln	Leu	Leu	Ala	Thr
				225				230				235			240
Ala	Leu	Cys	Thr	Glu	Leu	Cys	Asp	Asn	Leu	Ile	Ala	Gly	Gly	Val	Glu
				245				250				255			
Asp	Leu	His	Phe	Tyr	Thr	Leu	Asn	Arg	Pro	Gln	Met	Thr	Arg	Asp	Val
				260				265				270			
Cys	His	Ala	Leu	Gly	Val	Asn	Pro	Gly	Val	Val	Leu	Glu	Asn	Val	Ala
				275				280				285			

&lt;210&gt; 45

&lt;211&gt; 879

&lt;212&gt; DNA

&lt;213&gt; Neisseria meningitidis ser. A

&lt;220&gt;

<221> CDS  
<222> (1)..(876)  
<223> RNM00812

<400> 45  
 atg aat tac gca aaa gaa atc aat gcg tta aat aac agc ctt tcc gat 48  
 Met Asn Tyr Ala Lys Glu Ile Asn Ala Leu Asn Asn Ser Leu Ser Asp  
 1 5 10 15  
  
 ttg aaa ggc gac atc aac gtt tcg ttt gaa ttt ttt cca ccg aaa aac 96  
 Leu Lys Gly Asp Ile Asn Val Ser Phe Glu Phe Phe Pro Pro Lys Asn  
 20 25 30  
  
 gag caa atg gaa acg atg ctg tgg gat tcc atc cac cgt ctg caa acc 144  
 Glu Gln Met Glu Thr Met Leu Trp Asp Ser Ile His Arg Leu Gln Thr  
 35 40 45  
  
 ctg cat ccc aag ttc gta tcc gta acc tac ggc gca aac tcc ggc gaa 192  
 Leu His Pro Lys Phe Val Ser Val Thr Tyr Gly Ala Asn Ser Gly Glu  
 50 55 60  
  
 cgc gac cgc acg cac ggc atc gtc aaa cgc atc aaa cag gaa acc ggc 240  
 Arg Asp Arg Thr His Gly Ile Val Lys Arg Ile Lys Gln Glu Thr Gly  
 65 70 75 80  
  
 ttg gaa gca gca ccg cac ctg acc ggc atc gac gca tcc ccc gac gaa 288  
 Leu Glu Ala Ala Pro His Leu Thr Gly Ile Asp Ala Ser Pro Asp Glu  
 85 90 95  
  
 ttg cgc caa atc gcc aaa gac tat tgg gac agc ggc atc cgc cgc att 336  
 Leu Arg Gln Ile Ala Lys Asp Tyr Trp Asp Ser Gly Ile Arg Arg Ile  
 100 105 110  
  
 gtc gcc ctg cgt ggc gac gag ccg ccc ggt tat gag aaa aaa ccg ttt 384  
 Val Ala Leu Arg Gly Asp Glu Pro Pro Gly Tyr Glu Lys Lys Pro Phe  
 115 120 125  
  
 tac gcc gaa gac ttg gtt aag cta tta cgc tcc gtc gcc gac ttc gac 432  
 Tyr Ala Glu Asp Leu Val Lys Leu Leu Arg Ser Val Ala Asp Phe Asp  
 130 135 140  
  
 atc tct gtg gcg gca tat ccc gaa gtg cat ccc gaa gcc aaa tcc gca 480  
 Ile Ser Val Ala Ala Tyr Pro Glu Val His Pro Glu Ala Lys Ser Ala  
 145 150 155 160  
  
 caa gcc gat ctg att aat ctg aag cgc aaa atc gat gcg ggt gca aac 528  
 Gln Ala Asp Leu Ile Asn Leu Lys Arg Lys Ile Asp Ala Gly Ala Asn  
 165 170 175  
  
 cac gtc atc acc caa ttt ttc ttt gac gta gaa cgc tac ctg cgc ttc 576  
 His Val Ile Thr Gln Phe Phe Asp Val Glu Arg Tyr Leu Arg Phe  
 180 185 190  
  
 cgc gac cgc tgc gtg atg ttg ggt atc gat gtg gaa atc gtc cct ggt 624  
 Arg Asp Arg Cys Val Met Leu Gly Ile Asp Val Glu Ile Val Pro Gly  
 195 200 205  
  
 att ttg cct gtt acc aac ttc aag cag ctc ggc aaa atg gcg caa gta 672  
 Ile Leu Pro Val Thr Asn Phe Lys Gln Leu Gly Lys Met Ala Gln Val  
 210 215 220

acc aac gtc aaa atc cca agc tgg ctg tcg caa atg tat gaa ggt ttg	720
Thr Asn Val Lys Ile Pro Ser Trp Leu Ser Gln Met Tyr Glu Gly Leu	
225 230 235 240	
gac gac gac caa ggc acg cgc aac ctc gtc gcc gcc agt atc gcc atc	768
Asp Asp Asp Gln Gly Thr Arg Asn Leu Val Ala Ala Ser Ile Ala Ile	
245 250 255	
gat atg gtc aaa gtc ctg tcc cgc gaa ggc gtg aaa gat ttc cac ttc.	816
Asp Met Val Lys Val Leu Ser Arg Glu Gly Val Lys Asp Phe His Phe	
260 265 270	
tac acg ctc aac cgc agc gag ctg act tac gcc atc tgc cat att tta	864
Tyr Thr Leu Asn Arg Ser Glu Leu Thr Tyr Ala Ile Cys His Ile Leu	
275 280 285	
ggc gtg cgc cct taa	879
Gly Val Arg Pro	
290	

<210> 46	
<211> 292	
<212> PRT	
<213> Neisseria meningitidis ser. A	
<400> 46	
Met Asn Tyr Ala Lys Glu Ile Asn Ala Leu Asn Asn Ser Leu Ser Asp	
1 5 10 15	
Leu Lys Gly Asp Ile Asn Val Ser Phe Glu Phe Phe Pro Pro Lys Asn	
20 25 30	
Glu Gln Met Glu Thr Met Leu Trp Asp Ser Ile His Arg Leu Gln Thr	
35 40 45	
Leu His Pro Lys Phe Val Ser Val Thr Tyr Gly Ala Asn Ser Gly Glu	
50 55 60	
Arg Asp Arg Thr His Gly Ile Val Lys Arg Ile Lys Gln Glu Thr Gly	
65 70 75 80	
Leu Glu Ala Ala Pro His Leu Thr Gly Ile Asp Ala Ser Pro Asp Glu	
85 90 95	
Leu Arg Gln Ile Ala Lys Asp Tyr Trp Asp Ser Gly Ile Arg Arg Ile	
100 105 110	
Val Ala Leu Arg Gly Asp Glu Pro Pro Gly Tyr Glu Lys Lys Pro Phe	
115 120 125	
Tyr Ala Glu Asp Leu Val Lys Leu Leu Arg Ser Val Ala Asp Phe Asp	
130 135 140	
Ile Ser Val Ala Ala Tyr Pro Glu Val His Pro Glu Ala Lys Ser Ala	
145 150 155 160	
Gln Ala Asp Leu Ile Asn Leu Lys Arg Lys Ile Asp Ala Gly Ala Asn	
165 170 175	

His Val Ile Thr Gln Phe Phe Asp Val Glu Arg Tyr Leu Arg Phe  
 180 185 190  
 Arg Asp Arg Cys Val Met Leu Gly Ile Asp Val Glu Ile Val Pro Gly  
 195 200 205  
 Ile Leu Pro Val Thr Asn Phe Lys Gln Leu Gly Lys Met Ala Gln Val  
 210 215 220  
 Thr Asn Val Lys Ile Pro Ser Trp Leu Ser Gln Met Tyr Glu Gly Leu  
 225 230 235 240  
 Asp Asp Asp Gln Gly Thr Arg Asn Leu Val Ala Ala Ser Ile Ala Ile  
 245 250 255  
 Asp Met Val Lys Val Leu Ser Arg Glu Gly Val Lys Asp Phe His Phe  
 260 265 270  
 Tyr Thr Leu Asn Arg Ser Glu Leu Thr Tyr Ala Ile Cys His Ile Leu  
 275 280 285  
 Gly Val Arg Pro  
 290

<210> 47  
 <211> 849  
 <212> DNA  
 <213> *Campylobacter jejuni*

<220>  
 <221> CDS  
 <222> (1)...(846)  
 <223> RCJ02911

<400> 47  
 atg tgt agt ttt tct ttt gaa gtt ttt cca cca aga aag gat gaa aat 48  
 Met Cys Ser Phe Ser Phe Glu Val Phe Pro Pro Arg Lys Asp Glu Asn  
 1 5 10 15  
 atc aaa aat ctt cat gct atc tta gat gat tta ggg caa tta agc cct 96  
 Ile Lys Asn Leu His Ala Ile Leu Asp Asp Leu Gly Gln Leu Ser Pro  
 20 25 30  
 aat ttt atc agc gta acc ttt gga gct gga ggc tct att aac tca caa 144  
 Asn Phe Ile Ser Val Thr Phe Gly Ala Gly Gly Ser Ile Asn Ser Gln  
 35 40 45  
 aat act tta gaa gtt gca agc tta atc cag gaa gaa tat caa att cct 192  
 Asn Thr Leu Glu Val Ala Ser Leu Ile Gln Glu Glu Tyr Gln Ile Pro  
 50 55 60  
 agc ata gta cat tta cct tgc atc cat tct agt aaa gaa aaa atc act 240  
 Ser Ile Val His Leu Pro Cys Ile His Ser Ser Lys Glu Lys Ile Thr  
 65 70 75 80  
 cag ata ctt caa aaa tgc aaa gaa aaa aat ctt aat caa att ctt gcc 288  
 Gln Ile Leu Gln Lys Cys Lys Glu Lys Asn Leu Asn Gln Ile Leu Ala

85	90	95	
cta aga ggc gat ata tgt gaa aat tta aaa aaa agc aaa gat ttt tct			336
Leu Arg Gly Asp Ile Cys Glu Asn Leu Lys Lys Ser Lys Asp Phe Ser			
100	105	110	
tat gct agt gat tta att tct ttt ata aaa aaa caa gaa tac ttt gaa			384
Tyr Ala Ser Asp Leu Ile Ser Phe Ile Lys Lys Gln Glu Tyr Phe Glu			
115	120	125	
att tat gcc gca tgc tat ccc gaa aaa cat aat gaa tct aaa aat ttc			432
Ile Tyr Ala Ala Cys Tyr Pro Glu Lys His Asn Glu Ser Lys Asn Phe			
130	135	140	
atc gag gat ata cac cat ctt aaa act aag gta aat gca gga aca gat			480
Ile Glu Asp Ile His His Leu Lys Thr Lys Val Asn Ala Gly Thr Asp			
145	150	155	160
aag ctc att act caa ctt ttt tac gat aat gaa gat ttt tat act ttt			528
Lys Leu Ile Thr Gln Leu Phe Tyr Asp Asn Glu Asp Phe Tyr Thr Phe			
165	170	175	
aaa caa aat tgt gct tta gca gat att gac ata cct att tac gca ggt			576
Lys Gln Asn Cys Ala Leu Ala Asp Ile Asp Ile Pro Ile Tyr Ala Gly			
180	185	190	
att atg cct att act aac aaa aga cag gtt tta aaa att tct caa ctt			624
Ile Met Pro Ile Thr Asn Lys Arg Gln Val Leu Lys Ile Ser Gln Leu			
195	200	205	
tgc gga gct aaa atc cct cct aaa ttt gtt aaa att tta gaa aaa tat			672
Cys Gly Ala Lys Ile Pro Pro Lys Phe Val Lys Ile Leu Glu Lys Tyr			
210	215	220	
gaa aat aat act ttg gat tta gaa gat gca ggt atc gcg tat gct tgc			720
Glu Asn Asn Thr Leu Ala Leu Glu Asp Ala Gly Ile Ala Tyr Ala Cys			
225	230	235	240
gat caa att gtc gat tta atc aca agt ggt gta gat gga att cat ctt			768
Asp Gln Ile Val Asp Leu Ile Thr Ser Gly Val Asp Gly Ile His Leu			
245	250	255	
tat act atg aat aaa tcc aaa gcg gct att aaa att tat gaa gct gta			816
Tyr Thr Met Asn Lys Ser Lys Ala Ala Ile Lys Ile Tyr Glu Ala Val			
260	265	270	
aag cat ttg ctt aaa gaa gag ctt cat gct tag			849
Lys His Leu Leu Lys Glu Leu His Ala			
275	280		

<210> 48  
 <211> 282  
 <212> PRT  
 <213> *Campylobacter jejuni*

<400> 48  
 Met Cys Ser Phe Ser Phe Glu Val Phe Pro Pro Arg Lys Asp Glu Asn  
 1 5 10 15

Ile Lys Asn Leu His Ala Ile Leu Asp Asp Leu Gly Gln Leu Ser Pro  
 20 25 30

Asn Phe Ile Ser Val Thr Phe Gly Ala Gly Gly Ser Ile Asn Ser Gln  
 35 40 45

Asn Thr Leu Glu Val Ala Ser Leu Ile Gln Glu Glu Tyr Gln Ile Pro  
 50 55 60

Ser Ile Val His Leu Pro Cys Ile His Ser Ser Lys Glu Lys Ile Thr  
 65 70 75 80

Gln Ile Leu Gln Lys Cys Lys Glu Lys Asn Leu Asn Gln Ile Leu Ala  
 85 90 95

Leu Arg Gly Asp Ile Cys Glu Asn Leu Lys Lys Ser Lys Asp Phe Ser  
 100 105 110

Tyr Ala Ser Asp Leu Ile Ser Phe Ile Lys Lys Gln Glu Tyr Phe Glu  
 115 120 125

Ile Tyr Ala Ala Cys Tyr Pro Glu Lys His Asn Glu Ser Lys Asn Phe  
 130 135 140

Ile Glu Asp Ile His His Leu Lys Thr Lys Val Asn Ala Gly Thr Asp  
 145 150 155 160

Lys Leu Ile Thr Gln Leu Phe Tyr Asp Asn Glu Asp Phe Tyr Thr Phe  
 165 170 175

Lys Gln Asn Cys Ala Leu Ala Asp Ile Asp Ile Pro Ile Tyr Ala Gly  
 180 185 190

Ile Met Pro Ile Thr Asn Lys Arg Gln Val Leu Lys Ile Ser Gln Leu  
 195 200 205

Cys Gly Ala Lys Ile Pro Pro Lys Phe Val Lys Ile Leu Glu Lys Tyr  
 210 215 220

Glu Asn Asn Thr Leu Ala Leu Glu Asp Ala Gly Ile Ala Tyr Ala Cys  
 225 230 235 240

Asp Gln Ile Val Asp Leu Ile Thr Ser Gly Val Asp Gly Ile His Leu  
 245 250 255

Tyr Thr Met Asn Lys Ser Lys Ala Ala Ile Lys Ile Tyr Glu Ala Val  
 260 265 270

Lys His Leu Leu Lys Glu Glu Leu His Ala  
 275 280

<210> 49  
 <211> 852  
 <212> DNA  
 <213> Lactococcus lactis

<220>  
 <221> CDS  
 <222> (1)...(849)

<223> AAK05352

<400> 49  
 atg aca agt aat tcc aaa att ctt tct ttt gaa gtt ttt cca cct aca 48  
 Met Thr Ser Asn Ser Lys Ile Leu Ser Phe Glu Val Phe Pro Pro Thr  
 1 5 10 15  
  
 act caa att gga agt acc aac ttg gta aag acc ttg gat agc cta aga 96  
 Thr Gln Ile Gly Ser Thr Asn Leu Val Lys Thr Leu Asp Ser Leu Arg  
 20 25 30  
  
 act ctc tcg cca gat ttt atc agt gta act tgt agt aac aat aat tat 144  
 Thr Leu Ser Pro Asp Phe Ile Ser Val Thr Cys Ser Asn Asn Asn Tyr  
 35 40 45  
  
 gat aat att gga gat aca act ata aag ttt gct gat tat gta aac aat 192  
 Asp Asn Ile Gly Asp Thr Thr Ile Lys Phe Ala Asp Tyr Val Asn Asn  
 50 55 60  
  
 aca cta gat att cca gcg gtt gct cat tta cct gcc gct tat tta gat 240  
 Thr Leu Asp Ile Pro Ala Val Ala His Leu Pro Ala Ala Tyr Leu Asp  
 65 70 75 80  
  
 aaa gct caa gtg atc gaa att ttg gaa cgg tta aaa gat aaa caa atc 288  
 Lys Ala Gln Val Ile Glu Ile Leu Glu Arg Leu Lys Asp Lys Gln Ile  
 85 90 95  
  
 aaa aaa att ctt gct tta aga ggt gat atc agc gat gaa ccg atg aaa 336  
 Lys Lys Ile Leu Ala Leu Arg Gly Asp Ile Ser Asp Glu Pro Met Lys  
 100 105 110  
  
 gat gat ttt aaa ttt gca agt gat ttg gtt aaa ttt atc aaa gat tat 384  
 Asp Asp Phe Lys Phe Ala Ser Asp Leu Val Lys Phe Ile Lys Asp Tyr  
 115 120 125  
  
 gat gat agt ttt gaa gtt tta ggt gct tgc tac ccc gat att cat ccc 432  
 Asp Asp Ser Phe Glu Val Leu Gly Ala Cys Tyr Pro Asp Ile His Pro  
 130 135 140  
  
 gaa tca gta aat cga gtg agt gat ttt cat tat ctg aaa gaa aaa gta 480  
 Glu Ser Val Asn Arg Val Ser Asp Phe His Tyr Leu Lys Glu Lys Val  
 145 150 155 160  
  
 gat gct ggt tgt gac aga tta atc acg caa cta ttt ttt gat aat gat 528  
 Asp Ala Gly Cys Asp Arg Leu Ile Thr Gln Leu Phe Phe Asp Asn Asp  
 165 170 175  
  
 agt ttc tat gat ttt caa gaa cga tgc gca att gct gag ata aat act 576  
 Ser Phe Tyr Asp Phe Gln Glu Arg Cys Ala Ile Ala Glu Ile Asn Thr  
 180 185 190  
  
 ccg ata ttc gcc gga ata atg cca gta atc aat cga aat caa att ctt 624  
 Pro Ile Phe Ala Gly Ile Met Pro Val Ile Asn Arg Asn Gln Ile Leu  
 195 200 205  
  
 cgt cta tta aaa aat tgt aat acg cca tta cca gca aaa ttc att aga 672  
 Arg Leu Leu Lys Asn Cys Asn Thr Pro Leu Pro Ala Lys Phe Ile Arg  
 210 215 220  
  
 ata ctc gaa aaa tat gaa cat aat ctt atc gct tta agg gat gct gga 720

Ile Leu Glu Lys Tyr Glu His Asn Leu Ile Ala Leu Arg Asp Ala Gly  
 225 230 235 240

att gct tac gcc atc gat caa atc gtt gat tta gta aca gag gat gtt 768  
 Ile Ala Tyr Ala Ile Asp Gln Ile Val Asp Leu Val Thr Glu Asp Val  
 245 250 255

gct gga att cac ctc tat acg atg aat aat gca aat acg gca cac tcc 816  
 Ala Gly Ile His Leu Tyr Thr Met Asn Asn Ala Asn Thr Ala His Ser  
 260 265 270

atc cat gct tca att tct tct tta ttt acc ttt tga 852  
 Ile His Ala Ser Ile Ser Ser Leu Phe Thr Phe  
 275 280

<210> 50  
 <211> 283  
 <212> PRT  
 <213> Lactococcus lactis

<400> 50  
 Met Thr Ser Asn Ser Lys Ile Leu Ser Phe Glu Val Phe Pro Pro Thr  
 1 5 10 15

Thr Gln Ile Gly Ser Thr Asn Leu Val Lys Thr Leu Asp Ser Leu Arg  
 20 25 30

Thr Leu Ser Pro Asp Phe Ile Ser Val Thr Cys Ser Asn Asn Asn Tyr  
 35 40 45

Asp Asn Ile Gly Asp Thr Thr Ile Lys Phe Ala Asp Tyr Val Asn Asn  
 50 55 60

Thr Leu Asp Ile Pro Ala Val Ala His Leu Pro Ala Ala Tyr Leu Asp  
 65 70 75 80

Lys Ala Gln Val Ile Glu Ile Leu Glu Arg Leu Lys Asp Lys Gln Ile  
 85 90 95

Lys Lys Ile Leu Ala Leu Arg Gly Asp Ile Ser Asp Glu Pro Met Lys  
 100 105 110

Asp Asp Phe Lys Phe Ala Ser Asp Leu Val Lys Phe Ile Lys Asp Tyr  
 115 120 125

Asp Asp Ser Phe Glu Val Leu Gly Ala Cys Tyr Pro Asp Ile His Pro  
 130 135 140

Glu Ser Val Asn Arg Val Ser Asp Phe His Tyr Leu Lys Glu Lys Val  
 145 150 155 160

Asp Ala Gly Cys Asp Arg Leu Ile Thr Gln Leu Phe Phe Asp Asn Asp  
 165 170 175

Ser Phe Tyr Asp Phe Gln Glu Arg Cys Ala Ile Ala Glu Ile Asn Thr  
 180 185 190

Pro Ile Phe Ala Gly Ile Met Pro Val Ile Asn Arg Asn Gln Ile Leu

195

200

205

Arg Leu Leu Lys Asn Cys Asn Thr Pro Leu Pro Ala Lys Phe Ile Arg  
 210 215 220

Ile Leu Glu Lys Tyr Glu His Asn Leu Ile Ala Leu Arg Asp Ala Gly  
 225 230 235 240

Ile Ala Tyr Ala Ile Asp Gln Ile Val Asp Leu Val Thr Glu Asp Val  
 245 250 255

Ala Gly Ile His Leu Tyr Thr Met Asn Asn Ala Asn Thr Ala His Ser  
 260 265 270

Ile His Ala Ser Ile Ser Ser Leu Phe Thr Phe  
 275 280

<210> 51  
 <211> 891  
 <212> DNA  
 <213> Prochlorococcus maritima

<220>  
 <221> CDS  
 <222> (1)...(888)  
 <223> RCK01602

<400> 51  
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 Leu Lys Ser Lys Leu Gln Gln Thr Leu Glu Lys Asn Ser Lys Val Ile  
 1 5 10 15

aca gca gaa tta atg ccg cca aga gga gga gac ccc gta aga tct ctt 96  
 Thr Ala Glu Leu Met Pro Pro Arg Gly Gly Asp Pro Val Arg Ser Leu  
 20 25 30

aaa ata gca caa ctc ttg aga aat aag gtg cat gca gtt aat att aca 144  
 Lys Ile Ala Gln Leu Leu Arg Asn Lys Val His Ala Val Asn Ile Thr  
 35 40 45

gac gga agt aga gca ata atg aga atg tgt agt tta gca atg tct aaa 192  
 Asp Gly Ser Arg Ala Ile Met Arg Met Cys Ser Leu Ala Met Ser Lys  
 50 55 60

cta tta cta gac aat ggg ata gaa cct ata atg cag atc tca tgt aga 240  
 Leu Leu Leu Asp Asn Gly Ile Glu Pro Ile Met Gln Ile Ser Cys Arg  
 65 70 75 80

gat cgt aat aaa att gct tta caa tca gat att ctt gga gca aat gcc 288  
 Asp Arg Asn Lys Ile Ala Leu Gln Ser Asp Ile Leu Gly Ala Asn Ala  
 85 90 95

tta gga att aaa aat att tta tgc att aca gga gat tct gta aaa gcc 336  
 Leu Gly Ile Lys Asn Ile Leu Cys Ile Thr Gly Asp Ser Val Lys Ala  
 100 105 110

gga gat cag caa gaa aca aaa gcc gtt cat gaa ttt gag gca gta aga 384  
 Gly Asp Gln Gln Glu Thr Lys Ala Val His Glu Phe Glu Ala Val Arg  
 115 120 125

tta tta aaa caa att caa tca ttc aat caa gga att gat cct act ttt	432
Leu Leu Lys Gln Ile Gln Ser Phe Asn Gln Gly Ile Asp Pro Thr Phe	
130 135 140	
gaa caa ctt cca gac aaa agg act gaa att ttc tca ggt gcg gca gta	480
Glu Gln Leu Pro Asp Lys Arg Thr Glu Ile Phe Ser Gly Ala Ala Val	
145 150 155 160	
gat cca agt tgt cga aat caa aga agt tta aaa agt aga aca att aaa	528
Asp Pro Ser Cys Arg Asn Gln Arg Ser Leu Lys Ser Arg Thr Ile Lys	
165 170 175	
aaa aaa gag gcc ggt gca aat ttc tta caa act caa ata gtt atg gat	576
Lys Lys Glu Ala Gly Ala Asn Phe Leu Gln Thr Gln Ile Val Met Asp	
180 185 190	
aga aaa tgt tta gca gac ttt tgc aac gaa atc agt aat cca ctt gag	624
Arg Lys Cys Leu Ala Asp Phe Cys Asn Glu Ile Ser Asn Pro Leu Glu	
195 200 205	
ata cca gtt att gca gga gta ttt ctt tta aaa tca tat aaa aat gct	672
Ile Pro Val Ile Ala Gly Val Phe Leu Leu Lys Ser Tyr Lys Asn Ala	
210 215 220	
ctt ttc ata aat aaa ttt gta cct gga gcg aat att cct gaa aat gtt	720
Leu Phe Ile Asn Lys Phe Val Pro Gly Ala Asn Ile Pro Glu Asn Val	
225 230 235 240	
tta aat cgt ctc aaa gat gca aaa aat cca ctt caa gaa gga ata tta	768
Leu Asn Arg Leu Lys Asp Ala Lys Asn Pro Leu Gln Glu Gly Ile Leu	
245 250 255	
att gct tca gag caa gct caa gat ttt att aat att gca gat gga att	816
Ile Ala Ser Glu Gln Ala Gln Asp Phe Ile Asn Ile Ala Asp-Gly Ile	
260 265 270	
cat ctt atg gca gtc aaa tca gaa cat ctt atc cca gag ata ctt gaa	864
His Leu Met Ala Val Lys Ser Glu His Leu Ile Pro Glu Ile Leu Glu	
275 280 285	
aaa gct ggt ctc aat ctg gaa tgt taa	891
Lys Ala Gly Leu Asn Leu Glu Cys	
290 295	
<210> 52	
<211> 296	
<212> PRT	
<213> Prochlorococcus maritima	
<400> 52	
Leu Lys Ser Lys Leu Gln Gln Thr Leu Glu Lys Asn Ser Lys Val Ile	
1 5 10 15	
Thr Ala Glu Leu Met Pro Pro Arg Gly Gly Asp Pro Val Arg Ser Leu	
20 25 30	
Lys Ile Ala Gln Leu Leu Arg Asn Lys Val His Ala Val Asn Ile Thr	
35 40 45	

Asp Gly Ser Arg Ala Ile Met Arg Met Cys Ser Leu Ala Met Ser Lys  
 50 55 60

Leu Leu Leu Asp Asn Gly Ile Glu Pro Ile Met Gln Ile Ser Cys Arg  
 65 70 75 80

Asp Arg Asn Lys Ile Ala Leu Gln Ser Asp Ile Leu Gly Ala Asn Ala  
 85 90 95

Leu Gly Ile Lys Asn Ile Leu Cys Ile Thr Gly Asp Ser Val Lys Ala  
 100 105 110

Gly Asp Gln Gln Glu Thr Lys Ala Val His Glu Phe Glu Ala Val Arg  
 115 120 125

Leu Leu Lys Gln Ile Gln Ser Phe Asn Gln Gly Ile Asp Pro Thr Phe  
 130 135 140

Glu Gln Leu Pro Asp Lys Arg Thr Glu Ile Phe Ser Gly Ala Ala Val  
 145 150 155 160

Asp Pro Ser Cys Arg Asn Gln Arg Ser Leu Lys Ser Arg Thr Ile Lys  
 165 170 175

Lys Lys Glu Ala Gly Ala Asn Phe Leu Gln Thr Gln Ile Val Met Asp  
 180 185 190

Arg Lys Cys Leu Ala Asp Phe Cys Asn Glu Ile Ser Asn Pro Leu Glu  
 195 200 205

Ile Pro Val Ile Ala Gly Val Phe Leu Leu Lys Ser Tyr Lys Asn Ala  
 210 215 220

Leu Phe Ile Asn Lys Phe Val Pro Gly Ala Asn Ile Pro Glu Asn Val  
 225 230 235 240

Leu Asn Arg Leu Lys Asp Ala Lys Asn Pro Leu Gln Glu Gly Ile Leu  
 245 250 255

Ile Ala Ser Glu Gln Ala Gln Asp Phe Ile Asn Ile Ala Asp Gly Ile  
 260 265 270

His Leu Met Ala Val Lys Ser Glu His Leu Ile Pro Glu Ile Leu Glu  
 275 280 285

Lys Ala Gly Leu Asn Leu Glu Cys  
 290 295

<210> 53  
 <211> 1848  
 <212> DNA  
 <213> *Bacillus stearothermophilus*

<220>  
 <221> CDS  
 <222> (1)...(1845)  
 <223> RBE04103

<400> 53

gtg gga ttg ctg gat gag ttg aaa gag cgc att ctc atc gcc gac ggg	48
Val Gly Leu Leu Asp Glu Leu Lys Glu Arg Ile Leu Ile Ala Asp Gly	
1 5 10 15	
gcg atg gga acg ctt tta tat tcg cac ggc att gac cgt tgt ttt gaa	96
Ala Met Gly Thr Leu Leu Tyr Ser His Gly Ile Asp Arg Cys Phe Glu	
20 25 30	
gaa ttg aat cta tcc aat cca gat gaa atc gtc cat att cat gaa gcg	144
Glu Leu Asn Leu Ser Asn Pro Asp Glu Ile Val His Ile His Glu Ala	
35 40 45	
tat atc gcc gcg ggc gcc gac gtc att cag acg aat aca tac ggc gcc	192
Tyr Ile Ala Ala Gly Ala Asp Val Ile Gln Thr Asn Thr Tyr Gly Ala	
50 55 60	
aac tat gtg aaa ctc gcc cgc tac ggc ctt gaa gat gag gtg ccg gcc	240
Asn Tyr Val Lys Leu Ala Arg Tyr Gly Leu Glu Asp Glu Val Pro Ala	
65 70 75 80	
atc aac cgc gcg gtg cgg ctc gcc agg caa gcg gcg aac gga cgg	288
Ile Asn Arg Ala Ala Val Arg Leu Ala Arg Gln Ala Ala Asn Gly Arg	
85 90 95	
gca tac gtg ctc ggg acg atc ggg ggg ctg cgc acg tta aac aaa agc	336
Ala Tyr Val Leu Gly Thr Ile Gly Leu Arg Thr Leu Asn Lys Ser	
100 105 110	
gtc gtc acg ctc gaa gaa gtg aag cgg acg ttt cgc gag cag ctg ttt	384
Val Val Thr Leu Glu Val Lys Arg Thr Phe Arg Glu Gln Leu Phe	
115 120 125	
gtc ctg ctc gct gaa ggg gtc gac ggc gtg ctg ctc gag acg tat tac	432
Val Leu Ala Glu Gly Val Asp Gly Val Leu Leu Glu Thr Tyr Tyr	
130 135 140	
gat ttg gaa gag ttg gag acg gtg ctt gcc atc gcc cgc aaa gag acc	480
Asp Leu Glu Glu Leu Glu Thr Val Leu Ala Ile Ala Arg Lys Glu Thr	
145 150 155 160	
gac ttg ccg att atc gct cac gtc tcg ctc cat gaa gtc ggc gtc ttg	528
Asp Leu Pro Ile Ile Ala His Val Ser Leu His Glu Val Gly Val Leu	
165 170 175	
caa gat ggc acg ccg ctc gcg gac gcc ctt gcc cgc cta gag gcg ctc	576
Gln Asp Gly Thr Pro Leu Ala Asp Ala Leu Ala Arg Leu Glu Ala Leu	
180 185 190	
ggg gcc gat gtc gtc gga ctg aac tgt cgt ctc ggt cca tat cat atg	624
Gly Ala Asp Val Val Gly Leu Asn Cys Arg Leu Gly Pro Tyr His Met	
195 200 205	
ctt cgg tcg ctc gag gaa gtg ccg ctg cca aat cga gcg ttt ttg tcg	672
Leu Arg Ser Leu Glu Val Pro Leu Pro Asn Arg Ala Phe Leu Ser	
210 215 220	
gcg tat ccg aac gcc agc ctt ccg gat tac cgc gat ggg cgg ctt gtc	720
Ala Tyr Pro Asn Ala Ser Leu Pro Asp Tyr Arg Asp Gly Arg Leu Val	

225	230	235	240		
tat gag acg aac gct gaa tat ttc gag gaa acg gcc aaa gcg ttc cgc Tyr Glu Thr Asn Ala Glu Tyr Phe Glu Glu Thr Ala Lys Ala Phe Arg	245	250	255	768	
gac caa ggg gtg cgc ttg atc ggc ggg tgc tgc ggc acg acg ccg aaa Asp Gln Gly Val Arg Leu Ile Gly Gly Cys Cys Gly Thr Thr Pro Lys	260	265	270	816	
cat atc gaa gcg atg gca aaa gcg ctc tcc gac cga acg ccg gtg acg His Ile Glu Ala Met Ala Lys Ala Leu Ser Asp Arg Thr Pro Val Thr	275	280	285	864	
gaa aaa acg gtg aaa cgg cgc gcg gtg tct gta tca gtg caa gcg gag Glu Lys Thr Val Lys Arg Arg Ala Val Ser Val Ser Val Gln Ala Glu	290	295	300	912	
cgg ccc gcc cca tct ccc ctt ccc gag ctt gcc cgc acg cac cgc tcg Arg Pro Ala Pro Ser Pro Leu Pro Glu Leu Ala Arg Thr His Arg Ser	305	310	315	960	
gtc att gtg gag ctg gat ccg ccg aaa aaa ttg ggg att gac aag ttt Val Ile Val Glu Leu Asp Pro Pro Lys Lys Leu Gly Ile Asp Lys Phe	325	330	335	1008	
ctt gcc ggg gcg aaa gcg ctc cat gac gcc ggc atc gat gcg ctg acg Leu Ala Gly Ala Lys Ala Leu His Asp Ala Gly Ile Asp Ala Leu Thr	340	345	350	1056	
ttg gcc gac aac tcg ctc gcc acg ccg cgc atc agc aac gcc gct gtc Leu Ala Asp Asn Ser Leu Ala Thr Pro Arg Ile Ser Asn Ala Ala Val	355	360	365	1104	
gcc acg atc atc aag gag caa ctc ggc atc cgc ccg ctc gtg cat att Ala Thr Ile Ile Lys Glu Gln Leu Gly Ile Arg Pro Leu Val His Ile	370	375	380	1152	
aca tgc cgc gat cgc aat ttg atc ggc ttg cag tcg cat ttg atg ggc Thr Cys Arg Asp Arg Asn Leu Ile Gly Leu Gln Ser His Leu Met Gly	385	390	395	400	1200
ttg cat acg ctc ggc atc acc gat gtg ctc gcc att acc ggc gac ccg Leu His Thr Leu Gly Ile Thr Asp Val Leu Ala Ile Thr Gly Asp Pro	405	410	415	1248	
tcg aaa atc ggc gat ttt cca ggg gca acg tcc gtg tac gac tta tca Ser Lys Ile Gly Asp Phe Pro Gly Ala Thr Ser Val Tyr Asp Leu Ser	420	425	430	1296	
tcg ttc gat ttg atc cgc ttg atc cgc cag ttt aac gaa ggg ctg tcg Ser Phe Asp Leu Ile Arg Leu Ile Arg Gln Phe Asn Glu Gly Leu Ser	435	440	445	1344	
tac tcg ggc aaa ccg ctt ggg caa aaa acg aac ttc tcg atc ggc gct Tyr Ser Gly Lys Pro Leu Gly Gln Lys Thr Asn Phe Ser Ile Gly Ala	450	455	460	1392	
gcg ttc aac ccg aac gtc cgc cat ttg gac aaa gcg gtc gag ccg atg Ala Phe Asn Pro Asn Val Arg His Leu Asp Lys Ala Val Glu Arg Met				1440	

465	470	475	480	
gag aaa aaa atc caa tgc ggc gcc cat tat ttc ttg acc cag ccg att Glu Lys Lys Ile Gln Cys Gly Ala His Tyr Phe Leu Thr Gln Pro Ile 485		490		495
				1488
tac tcg gaa gag aaa atc gtt gaa gtg cac gaa gcg acc aag cat ctt Tyr Ser Glu Glu Lys Ile Val Glu Val His Glu Ala Thr Lys His Leu 500		505		510
				1536
gac acg ccg att tac atc ggc att atg ccg ctt gtg agc gcg cgc aac Asp Thr Pro Ile Tyr Ile Gly Ile Met Pro Leu Val Ser Ala Arg Asn 515		520		525
				1584
gcc gac ttt ttg cat cat gaa gtg ccg ggc att acg ctc tct gac gag Ala Asp Phe Leu His His Glu Val Pro Gly Ile Thr Leu Ser Asp Glu 530		535		540
				1632
att cgc gcc cgc atg gcc tgc agc ggc gac ccg gtg caa gca gcc Ile Arg Ala Arg Met Ala Ala Cys Ser Gly Asp Pro Val Gln Ala Ala 545		550		555
				1680
aag gaa ggc atc gct atc gcc aaa tcg ctc att gac gct gcg ttt gat Lys Glu Gly Ile Ala Ile Ala Lys Ser Leu Ile Asp Ala Ala Phe Asp 565		570		575
				1728
ttg ttt aac ggc att tat ttg atc acg ccg ttc ttg cgc tac gac atg Leu Phe Asn Gly Ile Tyr Leu Ile Thr Pro Phe Leu Arg Tyr Asp Met 580		585		590
				1776
acg gtc gag ctt gtc cgc tac att cac gaa aaa gaa gcg gcc gcc aaa Thr Val Glu Leu Val Arg Tyr Ile His Glu Lys Glu Ala Ala Ala Lys 595		600		605
				1824
•gaa agg aag gtt gtt cat ggc taa Glu Arg Lys Val Val His Gly 610		615		
				1848
<p>&lt;210&gt; 54  &lt;211&gt; 615  &lt;212&gt; PRT  &lt;213&gt; <i>Bacillus stearothermophilus</i></p>				
<p>&lt;400&gt; 54  Val Gly Leu Leu Asp Glu Leu Lys Glu Arg Ile Leu Ile Ala Asp Gly  1 5 10 15</p>				
<p>Ala Met Gly Thr Leu Leu Tyr Ser His Gly Ile Asp Arg Cys Phe Glu  20 25 30</p>				
<p>Glu Leu Asn Leu Ser Asn Pro Asp Glu Ile Val His Ile His Glu Ala  35 40 45</p>				
<p>Tyr Ile Ala Ala Gly Ala Asp Val Ile Gln Thr Asn Thr Tyr Gly Ala  50 55 60</p>				
<p>Asn Tyr Val Lys Leu Ala Arg Tyr Gly Leu Glu Asp Glu Val Pro Ala  65 70 75 80</p>				

Ile Asn Arg Ala Ala Val Arg Leu Ala Arg Gln Ala Ala Asn Gly Arg  
 85 90 95  
 Ala Tyr Val Leu Gly Thr Ile Gly Gly Leu Arg Thr Leu Asn Lys Ser  
 100 105 110  
 Val Val Thr Leu Glu Glu Val Lys Arg Thr Phe Arg Glu Gln Leu Phe  
 115 120 125  
 Val Leu Leu Ala Glu Gly Val Asp Gly Val Leu Leu Glu Thr Tyr Tyr  
 130 135 140  
 Asp Leu Glu Glu Leu Glu Thr Val Leu Ala Ile Ala Arg Lys Glu Thr  
 145 150 155 160  
 Asp Leu Pro Ile Ile Ala His Val Ser Leu His Glu Val Gly Val Leu  
 165 170 175  
 Gln Asp Gly Thr Pro Leu Ala Asp Ala Leu Ala Arg Leu Glu Ala Leu  
 180 185 190  
 Gly Ala Asp Val Val Gly Leu Asn Cys Arg Leu Gly Pro Tyr His Met  
 195 200 205  
 Leu Arg Ser Leu Glu Glu Val Pro Leu Pro Asn Arg Ala Phe Leu Ser  
 210 215 220  
 Ala Tyr Pro Asn Ala Ser Leu Pro Asp Tyr Arg Asp Gly Arg Leu Val  
 225 230 235 240  
 Tyr Glu Thr Asn Ala Glu Tyr Phe Glu Glu Thr Ala Lys Ala Phe Arg  
 245 250 255  
 Asp Gln Gly Val Arg Leu Ile Gly Gly Cys Cys Gly Thr Thr Pro Lys  
 260 265 270  
 His Ile Glu Ala Met Ala Lys Ala Leu Ser Asp Arg Thr Pro Val Thr  
 275 280 285  
 Glu Lys Thr Val Lys Arg Arg Ala Val Ser Val Ser Val Gln Ala Glu  
 290 295 300  
 Arg Pro Ala Pro Ser Pro Leu Pro Glu Leu Ala Arg Thr His Arg Ser  
 305 310 315 320  
 Val Ile Val Glu Leu Asp Pro Pro Lys Lys Leu Gly Ile Asp Lys Phe  
 325 330 335  
 Leu Ala Gly Ala Lys Ala Leu His Asp Ala Gly Ile Asp Ala Leu Thr  
 340 345 350  
 Leu Ala Asp Asn Ser Leu Ala Thr Pro Arg Ile Ser Asn Ala Ala Val  
 355 360 365  
 Ala Thr Ile Ile Lys Glu Gln Leu Gly Ile Arg Pro Leu Val His Ile  
 370 375 380  
 Thr Cys Arg Asp Arg Asn Leu Ile Gly Leu Gln Ser His Leu Met Gly  
 385 390 395 400

Leu His Thr Leu Gly Ile Thr Asp Val Leu Ala Ile Thr Gly Asp Pro  
 405 410 415  
 Ser Lys Ile Gly Asp Phe Pro Gly Ala Thr Ser Val Tyr Asp Leu Ser  
 420 425 430  
 Ser Phe Asp Leu Ile Arg Leu Ile Arg Gln Phe Asn Glu Gly Leu Ser  
 435 440 445  
 Tyr Ser Gly Lys Pro Leu Gly Gln Lys Thr Asn Phe Ser Ile Gly Ala  
 450 455 460  
 Ala Phe Asn Pro Asn Val Arg His Leu Asp Lys Ala Val Glu Arg Met  
 465 470 475 480  
 Glu Lys Lys Ile Gln Cys Gly Ala His Tyr Phe Leu Thr Gln Pro Ile  
 485 490 495  
 Tyr Ser Glu Glu Lys Ile Val Glu Val His Glu Ala Thr Lys His Leu  
 500 505 510  
 Asp Thr Pro Ile Tyr Ile Gly Ile Met Pro Leu Val Ser Ala Arg Asn  
 515 520 525  
 Ala Asp Phe Leu His His Glu Val Pro Gly Ile Thr Leu Ser Asp Glu  
 530 535 540  
 Ile Arg Ala Arg Met Ala Ala Cys Ser Gly Asp Pro Val Gln Ala Ala  
 545 550 555 560  
 Lys Glu Gly Ile Ala Ile Ala Lys Ser Leu Ile Asp Ala Ala Phe Asp  
 565 570 575  
 Leu Phe Asn Gly Ile Tyr Leu Ile Thr Pro Phe Leu Arg Tyr Asp Met  
 580 585 590  
 Thr Val Glu Leu Val Arg Tyr Ile His Glu Lys Glu Ala Ala Ala Lys  
 595 600 605  
 Glu Arg Lys Val Val His Gly  
 610 615

<210> 55  
 <211> 52  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> Description of the artificial sequence:PCR primer

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<210> 56  
 <211> 53  
 <212> DNA  
 <213> Artificial sequence

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<220>
<223> Description of the artificial sequence:PCR primer

<400> 56
tctagactcg agcggcccg cgccggcctt aaattgaaga cgaaagggcc tcg      53

<210> 57
<211> 47
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:PCR primer

<400> 57
gagatctaga cccggggatc cgctagcggg ctgctaaagg aagcggg      47

<210> 58
<211> 38
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:PCR primer

<400> 58
gagaggcgcg ccgctagcgt gggcgaagaa ctccagca      38

<210> 59
<211> 34
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:PCR primer

<400> 59
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<210> 60
<211> 34
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:PCR primer

<400> 60
gagagggcgg ccgctcaagt cggtaagcc acgc      34

<210> 61
<211> 140
<212> DNA
<213> Artificial sequence

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&lt;220&gt;

&lt;223&gt; Description of the artificial sequence:PCR primer

&lt;400&gt; 61

tcgaatttaa atctcgagag gcctgacgta	ggggccggta ccacgcgtca tatgactagt	60
tcggacctag ggatatcgta gacatcgatg	ctcttctgcg ttaattaaca attggatcc	120
tctagacccg ggatttaat		140

&lt;210&gt; 62

&lt;211&gt; 140

&lt;212&gt; DNA

&lt;213&gt; Artificial sequence

&lt;220&gt;

&lt;223&gt; Description of the artificial sequence:PCR primer

&lt;400&gt; 62

gatcatttaa atcccgggtc tagaggatcc caattgttaa ttaacgcaga agagcatcga	60
tgtcgacat atcccttagt ccgaactagt catatgacgc gtggtaccgg gcccgacgtc	120
aggcctctcg agatttaat	140

&lt;210&gt; 63

&lt;211&gt; 33

&lt;212&gt; DNA

&lt;213&gt; Artificial sequence

&lt;220&gt;

&lt;223&gt; Description of the artificial sequence:PCR primer

&lt;400&gt; 63

gagagcggcc gccgatcctt tttaacccat cac	33
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&lt;210&gt; 64

&lt;211&gt; 32

&lt;212&gt; DNA

&lt;213&gt; Artificial sequence

&lt;220&gt;

&lt;223&gt; Description of the artificial sequence:PCR primer

&lt;400&gt; 64

aggagcggcc gccatcgca ttttcttttgcg	32
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&lt;210&gt; 65

&lt;211&gt; 5091

&lt;212&gt; DNA

&lt;213&gt; Artificial sequence

&lt;220&gt;

&lt;223&gt; Description of the artificial sequence:plasmid

&lt;400&gt; 65

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tcttcgcaaa aatcgcccc tgcgcacgttgc gctcggtgc cgctgggtgc	180

gcttggcttg accgacttga tcagcggccg ctgcattaa atctcgagag gcctgacgtc 240  
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<210> 66  
 <211> 4323  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> Description of the artificial sequence: plasmid

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 ttttgataga acatgttaat cgatgtgtca tccgcattt taggatctcc ggctaattgca 420  
 aagacgtgt ggtagccgtg atagttgcg acagtgcgt cagcgttttga taatggccag 480  
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 tcagaaacctt gatatttttc attttttgc tggtcaggaa tttgcagcat atcatggcgt 600  
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 gga 4323

&lt;210&gt; 67

&lt;211&gt; 35

&lt;212&gt; DNA

&lt;213&gt; Artificial sequence

&lt;220&gt;

<223> Description of the artificial sequence: PCR Primer

<400> 67  
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<210> 68

<211> 34

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: PCR Primer

<400> 68  
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<210> 69

<211> 5860

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: plasmid

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aactgtcagc acgttagatcg aaaggtgcac aaaggtggcc ctggcgtac agaaatatgg 180

cggttcctcg cttgagagtg cgaaacgcatt tagaaacgtc gctgaacggat tcgttgccac 240

caagaaggct ggaaatgatg tcgtgggtgt ctgctccgca atgggagaca ccacggatga 300

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&lt;210&gt; 70

&lt;211&gt; 38

&lt;212&gt; DNA

&lt;213&gt; Artificial sequence

&lt;220&gt;

&lt;223&gt; Description of the artificial sequence: PCR Primer

&lt;400&gt; 70

cggcaccacc gacatcatct tcacctgccc tcgttccg

38

&lt;210&gt; 71

&lt;211&gt; 38

&lt;212&gt; DNA

&lt;213&gt; Artificial sequence

&lt;220&gt;

&lt;223&gt; Description of the artificial sequence: PCR Primer

&lt;400&gt; 71

cggaacgagg gcaggtgaag atgatgtcgg tggtgccg

38

&lt;210&gt; 72

&lt;211&gt; 1266

&lt;212&gt; DNA

&lt;213&gt; LysC mutant

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(1266)

&lt;400&gt; 72

gtg gcc ctg gtc gta cag aaa tat ggc ggt tcc tcg ctt gag agt gcg  
Val Ala Leu Val Val Gln Lys Tyr Gly Ser Ser Leu Glu Ser Ala  
1 5 10 15

48

gaa cgc att aga aac gtc gct gaa cgg atc gtt gcc acc aag aag gct  
Glu Arg Ile Arg Asn Val Ala Glu Arg Ile Val Ala Thr Lys Lys Ala  
20 25 30

96

gga aat gat gtc gtg gtt gtc tgc tcc gca atg gga gac acc acg gat  
Gly Asn Asp Val Val Val Cys Ser Ala Met Gly Asp Thr Thr Asp  
35 40 45

144

gaa ctt cta gaa ctt gca gcg gca gtg aat ccc gtt ccg cca gct cgt		192	
Glu Leu Leu Glu Leu Ala Ala Ala Val Asn Pro Val Pro Pro Ala Arg			
50	55	60	
gaa atg gat atg ctc ctg act gct ggt gag cgt att tct aac gct ctc		240	
Glu Met Asp Met Leu Leu Thr Ala Gly Glu Arg Ile Ser Asn Ala Leu			
65	70	75	80
gtc gcc atg gct att gag tcc ctt ggc gca gaa gcc caa tct ttc acg		288	
Val Ala Met Ala Ile Glu Ser Leu Gly Ala Glu Ala Gln Ser Phe Thr			
85	90	95	
ggc tct cag gct ggt gtg ctc acc acc gag cgc cac gga aac gca cgc		336	
Gly Ser Gln Ala Gly Val Leu Thr Thr Glu Arg His Gly Asn Ala Arg			
100	105	110	
att gtt gat gtc act cca ggt cgt gtg cgt gaa gca ctc gat gag ggc		384	
Ile Val Asp Val Thr Pro Gly Arg Val Arg Glu Ala Leu Asp Glu Gly			
115	120	125	
aag atc tgc att gtt gct ggt ttc cag ggt gtt aat aaa gaa acc cgc		432	
Lys Ile Cys Ile Val Ala Gly Phe Gln Gly Val Asn Lys Glu Thr Arg			
130	135	140	
gat gtc acc acg ttg ggt cgt ggt ggt tct gac acc act gca gtt gcg		480	
Asp Val Thr Thr Leu Gly Arg Gly Ser Asp Thr Thr Ala Val Ala			
145	150	155	160
ttg gca gct gct ttg aac gct gat gtg tgt gag att tac tcg gac gtt		528	
Leu Ala Ala Ala Leu Asn Ala Asp Val Cys Glu Ile Tyr Ser Asp Val			
165	170	175	
gac ggt gtg tat acc gct gac ccg cgc atc gtt cct aat gca cag aag		576	
Asp Gly Val Tyr Thr Ala Asp Pro Arg Ile Val Pro Asn Ala Gln Lys			
180	185	190	
ctg gaa aag ctc agc ttc gaa gaa atg ctg gaa ctt gct gct gtt ggc		624	
Leu Glu Lys Leu Ser Phe Glu Glu Met Leu Glu Leu Ala Ala Val Gly			
195	200	205	
tcc aag att ttg gtg ctg cgc agt gtt gaa tac gct cgt gca ttc aat		672	
Ser Lys Ile Leu Val Leu Arg Ser Val Glu Tyr Ala Arg Ala Phe Asn			
210	215	220	
gtg cca ctt cgc gta cgc tcg tct tat agt aat gat ccc ggc act ttg		720	
Val Pro Leu Arg Val Arg Ser Ser Tyr Ser Asn Asp Pro Gly Thr Leu			
225	230	235	240
att gcc ggc tct atg gag gat att cct gtg gaa gaa gca gtc ctt acc		768	
Ile Ala Gly Ser Met Glu Asp Ile Pro Val Glu Glu Ala Val Leu Thr			
245	250	255	
ggt gtc gca acc gac aag tcc gaa gcc aaa gta acc gtt ctg ggt att		816	
Gly Val Ala Thr Asp Lys Ser Glu Ala Lys Val Thr Val Leu Gly Ile			
260	265	270	
tcc gat aag cca ggc gag gct gcg aag gtt ttc cgt gcg ttg gct gat		864	
Ser Asp Lys Pro Gly Glu Ala Ala Lys Val Phe Arg Ala Leu Ala Asp			
275	280	285	

gca gaa atc aac att gac atg gtt ctg cag aac gtc tct tct gta gaa	912
Ala Glu Ile Asn Ile Asp Met Val Leu Gln Asn Val Ser Ser Val Glu	
290 295 300	
gac ggc acc acc gac atc atc ttc acc tgc cct cgt tcc gac ggc cgc	960
Asp Gly Thr Thr Asp Ile Ile Phe Thr Cys Pro Arg Ser Asp Gly Arg	
305 310 315 320	
cgc gcg atg gag atc ttg aag aag ctt cag gtt cag ggc aac tgg acc	1008
Arg Ala Met Glu Ile Leu Lys Lys Leu Gln Val Gln Gly Asn Trp Thr	
325 330 335	
aat gtg ctt tac gac gac cag gtc ggc aaa gtc tcc ctc gtg ggt gct	1056
Asn Val Leu Tyr Asp Asp Gln Val Gly Lys Val Ser Leu Val Gly Ala	
340 345 350	
ggc atg aag tct cac cca ggt gtt acc gca gag ttc atg gaa gct ctg	1104
Gly Met Lys Ser His Pro Gly Val Thr Ala Glu Phe Met Glu Ala Leu	
355 360 365	
cgc gat gtc aac gtg aac atc gaa ttg att tcc acc tct gag att cgt	1152
Arg Asp Val Asn Val Asn Ile Glu Leu Ile Ser Thr Ser Glu Ile Arg	
370 375 380	
att tcc gtg ctg atc cgt gaa gat gat ctg gat gct gct gca cgt gca	1200
Ile Ser Val Leu Ile Arg Glu Asp Asp Leu Asp Ala Ala Ala Arg Ala	
385 390 395 400	
ttg cat gag cag ttc cag ctg ggc ggc gaa gac gaa gcc gtc gtt tat	1248
Leu His Glu Gln Phe Gln Leu Gly Gly Glu Asp Glu Ala Val Val Tyr	
405 410 415	
gca ggc acc gga cgc taa	1266
Ala Gly Thr Gly Arg	
420	

<210> 73

<211> 421

<212> PRT

<213> LysC mutant

<400> 73

Val Ala Leu Val Val Gln Lys Tyr Gly Gly Ser Ser Leu Glu Ser Ala	
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Glu Arg Ile Arg Asn Val Ala Glu Arg Ile Val Ala Thr Lys Lys Ala	
20 25 30	

Gly Asn Asp Val Val Val Cys Ser Ala Met Gly Asp Thr Thr Asp	
35 40 45	

Glu Leu Leu Glu Leu Ala Ala Ala Val Asn Pro Val Pro Pro Ala Arg  
 50 55 60

Glu Met Asp Met Leu Leu Thr Ala Gly Glu Arg Ile Ser Asn Ala Leu  
 65 70 75 80

Val Ala Met Ala Ile Glu Ser Leu Gly Ala Glu Ala Gln Ser Phe Thr  
 85 90 95

Gly Ser Gln Ala Gly Val Leu Thr Thr Glu Arg His Gly Asn Ala Arg  
 100 105 110

Ile Val Asp Val Thr Pro Gly Arg Val Arg Glu Ala Leu Asp Glu Gly  
 115 120 125

Lys Ile Cys Ile Val Ala Gly Phe Gln Gly Val Asn Lys Glu Thr Arg  
 130 135 140

Asp Val Thr Thr Leu Gly Arg Gly Ser Asp Thr Thr Ala Val Ala  
 145 150 155 160

Leu Ala Ala Ala Leu Asn Ala Asp Val Cys Glu Ile Tyr Ser Asp Val  
 165 170 175

Asp Gly Val Tyr Thr Ala Asp Pro Arg Ile Val Pro Asn Ala Gln Lys  
 180 185 190

Leu Glu Lys Leu Ser Phe Glu Glu Met Leu Glu Leu Ala Ala Val Gly  
 195 200 205

Ser Lys Ile Leu Val Leu Arg Ser Val Glu Tyr Ala Arg Ala Phe Asn  
 210 215 220

Val Pro Leu Arg Val Arg Ser Ser Tyr Ser Asn Asp Pro Gly Thr Leu  
 225 230 235 240

Ile Ala Gly Ser Met Glu Asp Ile Pro Val Glu Glu Ala Val Leu Thr  
 245 250 255

Gly Val Ala Thr Asp Lys Ser Glu Ala Lys Val Thr Val Leu Gly Ile  
 260 265 270

Ser Asp Lys Pro Gly Glu Ala Ala Lys Val Phe Arg Ala Leu Ala Asp  
 275 280 285

Ala Glu Ile Asn Ile Asp Met Val Leu Gln Asn Val Ser Ser Val Glu  
 290 295 300

Asp Gly Thr Thr Asp Ile Ile Phe Thr Cys Pro Arg Ser Asp Gly Arg  
 305 310 315 320

Arg Ala Met Glu Ile Leu Lys Lys Leu Gln Val Gln Gly Asn Trp Thr  
 325 330 335

Asn Val Leu Tyr Asp Asp Gln Val Gly Lys Val Ser Leu Val Gly Ala  
 340 345 350

Gly Met Lys Ser His Pro Gly Val Thr Ala Glu Phe Met Glu Ala Leu  
 355 360 365

Arg Asp Val Asn Val Asn Ile Glu Leu Ile Ser Thr Ser Glu Ile Arg  
 370 375 380

Ile Ser Val Leu Ile Arg Glu Asp Asp Leu Asp Ala Ala Ala Arg Ala  
 385 390 395 400

Leu His Glu Gln Phe Gln Leu Gly Gly Glu Asp Glu Ala Val Val Tyr  
 405 410 415

Ala Gly Thr Gly Arg.  
 420

<210> 74

<211> 5860

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: plasmid

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 aactgtcagc acgttagatcg aaaggtgcac aaaggtggcc ctggtcgtac agaaatatgg 180  
 cggttcctcg cttgagagtg cggaacgcat tagaaacgtc gctgaacgga tcgttgccac 240

caagaaggct ggaaatgatg tcgtggtgt ctgctccgca atgggagaca ccacggatga	300
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<213> Artificial sequence

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<223> Description of the artificial sequence: PCR primer

<400> 75

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<212> DNA

<213> Artificial sequence

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<223> Description of the artificial sequence: PCR primer

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